

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:49:53 ; Search time 60 Seconds  
(without alignments)  
2316.890 Million cell updates/sec

Title: US-09-978-188a-7  
Perfect score: 2527  
Sequence: 1 MVKFPALHYWLRFLVPL.....TDMPTTEVTDIVEMREENE 492

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues  
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*  
1: GeneseqP1980s:\*  
2: GeneseqP1980s:\*  
3: GeneseqP2000s:\*  
4: GeneseqP2001s:\*  
5: GeneseqP2002s:\*  
6: GeneseqP2003as:\*  
7: GeneseqP2003bs:\*  
8: GeneseqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2527	100.0	492	2 AAY41686	Asy41686 Human PRO
2	2527	100.0	492	3 AAB44242	Ab44242 Human PRO
3	2527	100.0	492	5 AAU86135	Aau86135 Human PRO
4	2527	100.0	492	6 ABO25188	Abc25188 Novel hum
5	2527	100.0	492	6 ABU72194	Abu72194 Novel hum
6	2527	100.0	492	6 ABU84874	Abu84874 Human sec
7	2527	100.0	492	6 ABU61072	Abu61072 Human PRO
8	2527	100.0	492	6 ABU80341	Abu80341 Human sec
9	2527	100.0	492	6 ADA24546	Ada24546 Novel hum
10	2527	100.0	492	6 ABO19643	Abc19643 Novel hum
11	2527	100.0	492	6 ADA12207	Ada12207 Human sec
12	2527	100.0	492	6 ABO19534	Abc19534 Novel hum
13	2527	100.0	492	7 ADP73513	Adp73513 Human PRO
14	2527	100.0	492	7 ADP76229	Adp76229 Human PRO
15	2527	100.0	492	7 ADC36555	Adc36555 Human sec
16	2527	100.0	492	7 ADC61415	Adc61415 Human sec
17	2527	100.0	492	7 ADC63379	Adc63379 Human sec
18	2527	100.0	492	7 ADC66479	Adc66479 Human sec
19	2527	100.0	492	7 ADC68603	Adc68603 Human sec
20	2527	100.0	492	7 ADC62663	Adc62663 Human sec
21	2527	100.0	492	7 ADC67728	Adc67728 Human sec
22	2527	100.0	492	7 ADC41048	Adc41048 Human sec
23	2527	100.0	492	7 ADC67103	Adc67103 Human sec
24	2527	100.0	492	7 ADC62039	Adc62039 Human sec
25	2527	100.0	492	7 ADC41672	Adc41672 Human sec

26	2527	100.0	492	7 ADE49041	Ade49041 Human sec
27	2527	100.0	492	7 ADE35095	Ade35095 Human sec
28	2527	100.0	492	7 ADE16209	Ade16209 Human sec
29	2527	100.0	492	7 ADD72824	Add72824 Human sec
30	2527	100.0	492	7 ADD72182	Add72182 Human sec
31	2527	100.0	492	7 ADE16833	Ade16833 Human sec
32	2527	100.0	492	8 ADE48341	Ade48341 Human sec
33	2527	100.0	492	8 ADE89442	Ade89442 Human sec
34	2527	99.8	492	4 AAU05581	Aau05581 Human pro
35	2522	99.8	492	5 ABB98306	Abb98306 Human ANK
36	2522	99.8	492	6 ABR57487	AbR57487 Human ANK
37	2514	99.5	492	5 ABB98316	Abb98316 Human ANK
38	2511.5	99.4	493	5 ABB98315	Abb98315 Human ANK
39	2510	99.3	492	5 ABB98312	Abb98312 Human ANK
40	2508	99.2	492	5 ABB98311	Abb98311 Human ANK
41	2507.5	99.1	491	5 ABB98313	Abb98313 Human ANK
42	2505.5	99.1	491	5 ABB98314	Abb98314 Human ANK
43	2502	99.0	492	4 AAU05582	Aau05582 Mouse pro
44	2502	99.0	492	5 ABB98307	Abb98307 Mouse ANK
45	2345	92.8	467	4 AAM40539	Aam40539 Human pol

ALIGNMENTS

RESULT 1  
AAY41686  
ID AAY41686 standard; protein; 492 AA.  
XX

AC AAY41686;  
XX

DT 07-DEC-1999 (first entry)  
XX

DE Human PRO274 protein sequence.  
XX

XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein.  
XX

OS Homo sapiens.  
XX

PN WO9946281-A2.  
XX

PD 16-SEP-1999.  
XX

PF 08-MAR-1999; 99WO-US005028.  
XX

PR 10-MAR-1998; 98US-0077450P.  
PR

PR 11-MAR-1998; 98US-0077632P.  
PR

PR 11-MAR-1998; 98US-0077641P.  
PR

PR 11-MAR-1998; 98US-0077649P.  
PR

PR 12-MAR-1998; 98US-0077791P.  
PR

PR 13-MAR-1998; 98US-0078004P.  
PR

PR 17-MAR-1998; 98US-00040220.  
PR

PR 20-MAR-1998; 98US-0078886P.  
PR

PR 20-MAR-1998; 98US-0078910P.  
PR

PR 20-MAR-1998; 98US-0078936P.  
PR

PR 20-MAR-1998; 98US-0078939P.  
PR

PR 25-MAR-1998; 98US-0079294P.  
PR

PR 26-MAR-1998; 98US-0079656P.  
PR

PR 27-MAR-1998; 98US-0079663P.  
PR

PR 27-MAR-1998; 98US-0079689P.  
PR

PR 27-MAR-1998; 98US-0079728P.  
PR

PR 27-MAR-1998; 98US-0079786P.  
PR

PR 30-MAR-1998; 98US-0079920P.  
PR

PR 30-MAR-1998; 98US-0079923P.  
PR

PR 31-MAR-1998; 98US-0080105P.  
PR

PR 31-MAR-1998; 98US-0080107P.  
PR

PR 31-MAR-1998; 98US-0080165P.  
PR

PR 31-MAR-1998; 98US-0080194P.  
PR

PR 01-APR-1998; 98US-0080327P.  
PR

PR 01-APR-1998; 98US-0080328P.  
PR

PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 08-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 05-MAY-1998; 98US-0084414P.  
PR 05-MAY-1998; 98US-0084441P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085589P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086466P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.  
PR (GETH ) GENENTECH INC.  
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
PI WPI; 1999-551358/46.  
DR N-PSDB; AAZ33895.  
XX New secreted and transmembrane polypeptides and their polynucleotides,  
PI useful for treating blood coagulation disorders, cancers and cellular  
PI adhesion disorders.

XX Claim 12; Fig 4; 530pp; English.  
XX The present invention describes secreted and transmembrane polypeptides  
CC and their polynucleotides. The nucleotide sequences are useful as sources  
CC of probes, primers, for chromosome mapping, and for generation of  
CC antisense sequences. They can also be used to create transgenic animals.  
CC The proteins can be used to treat a variety of diseases and disorders,  
CC depending on their function. Diseases that may be treated include blood  
CC coagulation disorders, cancers and cellular adhesion disorders. They may  
CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to  
CC AAY41774 represent polynucleotide and polypeptide sequence given in the  
CC exemplification of the present invention  
XX SQ Sequence 492 AA;

Query Match 100.0%; Score 2527; DB 2; Length 492;  
Best Local Similarity 100.0%; Pred. No. 1.4e-285;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MVRFPALTHYWPILRLVPLGLITNIALDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
Db 1 MVRFPALTHYWPILRLVPLGLITNIALDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
Qy 61 FFTGPMDSDFKNVGLVFNYSKRDRTKAVLCMVVAGIAAFAVHTLIAYSDGLGYIINKLHV 120  
Db 61 FFTGPMDSDFKNVGLVFNYSKRDRTKAVLCMVVAGIAAFAVHTLIAYSDGLGYIINKLHV 120  
Qy 121 DESVGSKTRAFILYLAAPPMDAMWATHAGILKHKYSFLVGCASISDVIAQVVFVAILL 180  
Db 121 DESVGSKTRAFILYLAAPPMDAMWATHAGILKHKYSFLVGCASISDVIAQVVFVAILL 180  
Qy 181 HSHLECREPLILPILSLYMGALVRCITTLCLGYGYNKIHDIIPDRSGPELGDAIRKMLSF 240  
Db 181 HSHLECREPLILPILSLYMGALVRCITTLCLGYGYNKIHDIIPDRSGPELGDAIRKMLSF 240  
Qy 241 WPLALILATQISRPITVNFVSRDLGGSSAAEAVALTATYVGHMPYGMWTEIRAVY 300  
Db 241 WPLALILATQISRPITVNFVSRDLGGSSAAEAVALTATYVGHMPYGMWTEIRAVY 300  
Qy 301 PAFDKNPNKLVSTNTVTAHKKFTFVCMALSLTLCFVMTWPNVSEKILIDIIIGVD 360  
Db 301 PAFDKNPNKLVSTNTVTAHKKFTFVCMALSLTLCFVMTWPNVSEKILIDIIIGVD 360  
Qy 361 FAFALCVPLRIPSPFPVPTVRAHLTGWIMTLKKTFLVLAAPSVLRIIVLIASLVLPY 420  
Db 361 FAFALCVPLRIPSPFPVPTVRAHLTGWIMTLKKTFLVLAAPSVLRIIVLIASLVLPY 420  
Qy 421 LGVHGATLGVGSLLAGFVGSTWVAIAACVYRKQKKMENESATEGEDSAMTDMPTTE 480  
Db 421 LGVHGATLGVGSLLAGFVGSTWVAIAACVYRKQKKMENESATEGEDSAMTDMPTTE 480  
Qy 481 VTDIVEMRENE 492  
Db 481 VTDIVEMRENE 492

RESULT 2  
AAB44242  
ID AAB44242 standard; protein; 492 AA.  
XX AAB44242;  
XX  
XX 08-FEB-2001 (first entry)  
XX Human PRO274 (UNQ241) protein sequence SEQ ID NO:7.  
XX Human; secreted protein; transmembrane protein; PRO; EST; cyrostatic;  
XX expressed sequence tag; detection; cancer.  
XX Homo sapiens.  
XX WO200053756-A2.  
PN

XX PD 14-SEP-2000.  
XX PF 18-FEB-2000; 2000WO-US004341.  
XX PR 08-MAR-1999; 99WO-US005028.  
XX PR 12-MAR-1999; 99US-0123957P.  
XX PR 29-MAR-1999; 99US-0126773P.  
XX PR 21-APR-1999; 99US-0130232P.  
XX PR 28-APR-1999; 99US-0131445P.  
XX PR 14-MAY-1999; 99US-0134287P.  
XX PR 23-JUN-1999; 99US-0141037P.  
XX PR 26-JUL-1999; 99US-0145698P.  
XX PR 29-OCT-1999; 99US-0162506P.  
XX PR 30-NOV-1999; 99WO-US028313.  
XX PR 02-DEC-1999; 99WO-US028551.  
XX PR 02-DEC-1999; 99WO-US028565.  
XX PR 16-DEC-1999; 99WO-US030095.  
XX PR 30-DEC-1999; 99WO-US031243.  
XX PR 30-DEC-1999; 99WO-US031274.  
XX PR 05-JAN-2000; 2000WO-US000219.  
XX PR 06-JAN-2000; 2000WO-US000277.  
XX PR 06-JAN-2000; 2000WO-US000376.  
XX PA (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
XX PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
XX PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
XX PI Stewart TA, Tumas D, Williams PM, Wood WI;  
XX DR WPI; 2000-611443/58.  
XX DR N-PSDB; AAC78459.  
XX PT Novel PRO polypeptides and polynucleotides used in detection methods, to  
XX PT target bioactive molecules to specific cells, and to modulate cellular  
XX PT activities.  
XX PS Claim 12; Fig 4; 636pp; English.  
XX CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence  
XX CC tag) sequences which encode secreted or transmembrane PRO polypeptides.  
XX CC The PRO polynucleotides and polypeptides have cytostatic activity. The  
XX CC polynucleotides and polypeptides can be used for detecting the presence  
XX CC of PRO polypeptides in samples, for linking bioactive molecules to cells  
XX CC and for modulating biological activities of cells, using the polypeptides  
XX CC for specific targeting. The polypeptide targeting can be used to kill the  
XX CC target cells, e.g. for the treatment of cancers. The polypeptide pairs  
XX CC provide specific targeting of bioactive molecules to cells. AAC78600 to  
XX CC AAC78987 represent PCR primers and probes used in the isolation of the  
XX CC PRO polynucleotide sequences  
XX SQ Sequence 492 AA;  
Query Match 100.0%; Score 2527; DB 3; Length 492;  
Best Local Similarity 100.0%; Pred. No. 1.4e-285;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MYKFPALHYWPLIPLVPLGLTNTAIDPGEQALNARGIAAVKEDAVEMLASGLAYSLMK 60  
DB 1 MYKFPALHYWPLIPLVPLGLTNTAIDPGEQALNARGIAAVKEDAVEMLASGLAYSLMK 60  
QY 61 FTGPMDSDFKNGVNFVNSKRDTRKAVLCMVVAGAIAAVFTLTIAYSDLGYYIINKLHV 120  
DB 61 FTGPMDSDFKNGVNFVNSKRDTRKAVLCMVVAGAIAAVFTLTIAYSDLGYYIINKLHV 120  
QY 121 DESVGSKTRAFLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQWVFAILL 180  
DB 121 DESVGSKTRAFLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQWVFAILL 180  
QY 181 HSHLECREPLLIPILSYMGALVRCUTTLCLGYVKNHDIIPDRSGPELGGDATIRKMLSF 240

DB 181 HSHLECREPLLIPILSYMGALVRCUTTLCLGYVKNHDIIPDRSGPELGGDATIRKMLSF 240  
QY 241 WWPLALILATORISRPVNLVFSRD:GGSSAATEAVAILTATYPVGHMPYGLWTEIRAY 300  
DB 241 WWPLALILATORISRPVNLVFSRD:GGSSAATEAVAILTATYPVGHMPYGLWTEIRAY 300  
QY 301 PAFDKNPNKLVSTNTVTAHHIKFTFVCMWALSITLCTCFVMTDNPVSEKILIDIIGVD 360  
DB 301 PAFDKNPNKLVSTNTVTAHHIKFTFVCMWALSITLCTCFVMTDNPVSEKILIDIIGVD 360  
QY 361 FAFAEICVWPLRIFSPFPVTVRAHITGMLWTLKKTFTVLAPSSVLRIIVLIASLVLPY 420  
DB 361 FAFAEICVWPLRIFSPFPVTVRAHITGMLWTLKKTFTVLAPSSVLRIIVLIASLVLPY 420  
QY 421 LGVHGATLGVGSLLAGFVGESTWVAIAACYVYRKQKKOMENESATEGEDSAMTDPPTTE 480  
DB 421 LGVHGATLGVGSLLAGFVGESTWVAIAACYVYRKQKKOMENESATEGEDSAMTDPPTTE 480  
QY 481 VTDIVEMRENE 492  
DB 481 VTDIVEMRENE 492  
RESULT 3  
AAU86135  
ID AAU86135 standard; protein; 492 AA.  
XX AC AAU86135;  
XX DT 15-JUL-2002 (first entry)  
XX DE Human PRO274 polypeptide.  
XX KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;  
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;  
KW neuroprotective.  
XX OS Homo sapiens.  
XX FN WO200153486-A1.  
XX PD 26-JUL-2001.  
XX PF 11-FEB-2000; 2000WO-US003565.  
XX PR 08-MAR-1999; 99WO-US005028.  
XX PR 11-MAR-1999; 99US-0123972P.  
XX PR 11-MAY-1999; 99US-0133459P.  
XX PR 02-JUN-1999; 99WO-US012252.  
XX PR 22-JUN-1999; 99US-0140650P.  
XX PR 22-JUN-1999; 99US-0140653P.  
XX PR 20-JUL-1999; 99US-014758P.  
XX PR 26-JUL-1999; 99US-0145698P.  
XX PR 28-JUL-1999; 99US-0146222P.  
XX PR 17-AUG-1999; 99US-0149395P.  
XX PR 31-AUG-1999; 99US-0151689P.  
XX PR 01-SEP-1999; 99WO-US020111.  
XX PR 15-SEP-1999; 99WO-US021090.  
XX PR 30-NOV-1999; 99WO-US028313.  
XX PR 01-DEC-1999; 99WO-US028301.  
XX PR 01-DEC-1999; 99WO-US028634.  
XX PR 05-JAN-2000; 2000WO-US000219.  
XX (GETH ) GENENTECH INC.  
XX PA Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
XX PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
XX PI Watanabe CK, Wood WI;  
XX DR WPI; 2002-205567/26.  
XX DR N-PSDB; ABK40261.

PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
PT benign or malignant tumors, leukemias and lymphoid malignancies,  
PT inflammatory, angiogenic and immunologic disorders.  
XX  
XX  
PS Claim 61; Fig 16; 302pp; English.

XX  
CC The present invention relates to the isolation of novel human PRO  
CC polypeptides and the polynucleotide sequences encoding them. The PRO  
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for  
CC treating benign or malignant tumors (e.g. renal, kidney, bladder,  
CC breast, etc), leukemias and lymphoid malignancies, other disorders such  
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,  
CC stromal and blastocoeleic disorders, inflammatory, immune and angiogenic  
CC disorders. The polynucleotide sequences are also useful in gene therapy.  
CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention  
XX  
SQ Sequence 492 AA;

Query Match 100.0%; Score 2527; DB 5; Length 492;  
Best Local Similarity 100.0%; Pred. No. 1.4e-285;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKVEPALTHYWPILRFVLPGITNIAIDFGQALNRGIAAVKEDAVEMLASGLAYSLMK 60  
DB 1 MKVEPALTHYWPILRFVLPGITNIAIDFGQALNRGIAAVKEDAVEMLASGLAYSLMK 60  
QY 61 FFGPMDSDFKNGVLGVFVNSKRDRTKAVLCMVAGATAAVERHTLIAYSDGLGYIINKLHV 120  
DB 61 FFGPMDSDFKNGVLGVFVNSKRDRTKAVLCMVAGATAAVERHTLIAYSDGLGYIINKLHV 120  
QY 121 DESVGSKTRAFYLAAPFPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
DB 121 DESVGSKTRAFYLAAPFPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
QY 181 HSHLECPRLIPILSYMGALVRCCTTCLGYKNHDIIDPDRSGPBGDGIIRKWLSP 240  
DB 181 HSHLECPRLIPILSYMGALVRCCTTCLGYKNHDIIDPDRSGPBGDGIIRKWLSP 240  
QY 241 WWPALILATORISRPVNLVFSRDLGSSAATEAVAILTATVPVGHMPYGLTEIRAVY 300  
DB 241 WWPALILATORISRPVNLVFSRDLGSSAATEAVAILTATVPVGHMPYGLTEIRAVY 300  
QY 301 PAFKNNPSNKLVTSTNTVTAHKKFTFVCMALSLTLCFVMTFVNSKILIDIIGVD 360  
DB 301 PAFKNNPSNKLVTSTNTVTAHKKFTFVCMALSLTLCFVMTFVNSKILIDIIGVD 360  
QY 361 PAFALCVVPLRIFSEPPVPTVRAHLTGWMTLTKTFVLAPSSVLRILVILASLVLPY 420  
DB 361 PAFALCVVPLRIFSEPPVPTVRAHLTGWMTLTKTFVLAPSSVLRILVILASLVLPY 420  
QY 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYYVRKQKKMENESATEGEDSAMTDPTEE 480  
DB 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYYVRKQKKMENESATEGEDSAMTDPTEE 480  
QY 481 VTDIVEMRENE 492  
DB 481 VTDIVEMRENE 492

RESULT 4  
ASO25188  
ID ABO25188 standard; protein; 492 AA.  
XX  
XX ABO25188;  
AC  
DT 09-SEP-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO274.  
XX  
KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;  
KW cell death; growth induction cascade; blood coagulation cascade;  
KW viral infection.  
XX

OS Homo sapiens.  
XX  
PN US2003050239-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 15-OCT-2001; 2001US-00978191.  
XX  
PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 10-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079566P.  
PR 27-MAR-1998; 98US-0079663P.  
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PR 05-JAN-2000; 2000US-0000219.
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PR 17-MAY-2000; 2000US-0013705.
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PR 02-JUN-2000; 2000US-0015264.
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PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00817092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-0017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001US-0019692.
PR 29-JUN-2001; 2001US-0021066.
PR 03-JUL-2001; 2001US-0021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Rotstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 100.0%; Score 2527; DB 6; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.4e-285;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 FFTGPMDFKNGVLVFNKRDRTKAVLCMVVAGNIAAVFHTLIAYSDLGYYIINKLHV 120
Db 61 FFTGPMDFKNGVLVFNKRDRTKAVLCMVVAGNIAAVFHTLIAYSDLGYYIINKLHV 120
Qy 121 DESVGSKTRRAFLYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180
Db 121 DESVGSKTRRAFLYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180
Qy 181 HSHLECREPLIPILSLYNGALVRCITICLYGKYNHDIIPDRSGPELGGATIRKMLSF 240
Db 181 HSHLECREPLIPILSLYNGALVRCITICLYGKYNHDIIPDRSGPELGGATIRKMLSF 240
Qy 241 WMPALILATQIRISRPVNLFSVRDLGGSSAATEAVAILTATYPVGHMPYGLWTEIRAVY 300
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QY 481 VTDIVEMREENE 492

Db 481 VTDIVEMREENE 492

RESULT 5

ABU72194

ID ABU72194 standard; protein; 492 AA.

XX AC ABU72194;

XX DT 16-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO274.

XX DE Human; secreted and transmembrane protein; PRO; antiinflammatory;

KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;

KW antidiabetic; gene therapy; inflammatory disease; organ failure;

KW atherosclerosis; cardiac injury; infertility; birth defect;

KW premature aging; AIDS; cancer; diabetic complication; chromosome mapping;

KW gene mapping; pharmaceutical; diagnostic; biosensor; bioreactor;

KW tissue typing.

XX OS Homo sapiens.

XX PN US2002192706-A1.

XX PD 19-DEC-2002.

XX PF 24-OCT-2001; 2001US-00999832.

XX PR 17-OCT-1997; 97US-0062250P.

PR 13-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066364P.

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PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 12-MAR-1998; 98US-0077791P.

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PR 27-MAR-1998; 98US-0079786P.

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PR 30-MAR-1998; 98US-0079923P.

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PR 01-APR-1998; 98US-0080328P.

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PR 01-APR-1998; 98US-0080349P.

PR 08-APR-1998; 98US-0081049P.

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PR 08-APR-1998; 98US-0081071P.

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PR 09-APR-1998; 98US-0081229P.

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PR 22-APR-1998; 98US-0082804P.

PR 23-APR-1998; 98US-0082796P.

PR 07-OCT-1998; 98WO-US021141.

PR 20-NOV-1998; 98WO-US024855.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.

PR 14-MAY-1999; 99WO-US010733.

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PR 02-DEC-1999; 99WO-US028551.

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PR 30-DEC-1999; 99WO-US031243.

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PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

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PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

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PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

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PR 02-JUN-2000; 2000WO-US015264.

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PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021086.

PR 09-JUL-2001; 2001WO-US021735.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;

XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;

PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;

PI Stewart TA, Tumas D, Williams PM, Wood WI;

XX WPI; 2003-328860/31.

DR N-PSDB; ACA63463.

XX New secreted and transmembrane nucleic acids and polypeptides, designated

PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,

PT cardiac injury, infertility, birth defects, premature aging, AIDS, or

PT cancer.

XX Claim 12; Fig 4; 453pp; English.

PS The invention describes an isolated nucleic acid (I) comprising, or which

CC is at least 80 % sequence identity to, or the full-length coding sequence



PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015284.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000US-00709238.  
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 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
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 PR 01-JUN-2001; 2001US-00872035.  
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 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 30-JUL-2001; 2001US-00918585.  
 XX  
 PA (GETH) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
 PI Stewart TA, Tumas D, Williams PM, Wood W;  
 XX  
 DR WPI: 2003-328499/31.  
 DR N-PSDB; ACA71627.  
 XX  
 PT New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as  
 PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying  
 PT modulators of receptor-ligand interactions.  
 XX  
 PS Claim 12; SEQ ID NO 7; 55pp; English.  
 XX  
 CC The invention relates to an isolated secreted and transmembrane  
 CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful  
 CC in PRO polypeptide detection methods. The PRO polypeptide is useful for  
 CC linking a bioactive molecule to a cell. The PRO polypeptide or an  
 CC antibody against it is useful for modulating a biological activity of a  
 CC cell. The PRO polypeptide is useful in industrial applications including  
 CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO  
 CC polypeptide is also useful as a thrombolytic agent, interferon,  
 CC interleukin, erythropoietin, colony stimulating factor and other  
 CC cytokines. The PRO polypeptide is useful for treating disease such as  
 CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,  
 CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,  
 CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,  
 CC Parkinson's disease; cardiovascular disease e.g. hypertension and  
 CC myocardial ischaemia; kidney disease e.g. renal failure and  
 CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial  
 CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory  
 CC bowel disease; reproductive disorders e.g. premature labour and  
 CC pre-eclampsia; carcinogenesis. The present sequence represents the amino  
 CC acid sequence of a PRO polypeptide of the invention. Note: The sequence  
 CC data for this patent did not form part of the printed specification but  
 CC was obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20020177553  
 XX  
 SQ Sequence 492 AA;

Query Match 100.0%; Score 2527; DB 6; Length 492;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-285;  
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB |||||  
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 DB |||||  
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 DB |||||  
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 DB |||||  
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 XX AC ASU61072;  
 XX AC ASU61072;  
 DT 08-MAY-2003 (first entry)  
 XX Human PRO274 polypeptide.  
 XX Human; PRO polypeptide; secreted and transmembrane protein;  
 KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;  
 KW cardiac insufficiency; nervous system disorder; kidney disorder;  
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;  
 KW genetic disorder; cytostatic; antidiabetic; antinflammatory;  
 KW antiarthritic; anti-tumour; vulnary; antianaemic; dermatological;  
 KW cardiant.  
 OS Homo sapiens.  
 XX US2002169284-A1.  
 XX 14-NOV-2002.  
 PD 16-OCT-2001; 2001US-00978697.  
 XX 26-MAY-1981; 81US-00267213.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 03-NOV-1997; 97US-0064249P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 21-NOV-1997; 97US-0066364P.  
 PR 11-MAR-1998; 98US-0077450P.  
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 PR 11-MAR-1998; 98US-0077649P.  
 PR 12-MAR-1998; 98US-0077791P.

13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 25-MAR-1998; 98US-0079566P.  
PR 27-MAR-1998; 98US-0079564P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 26-JUN-1998; 98US-00105413.  
PR 07-OCT-1998; 98US-00168978.  
PR 07-OCT-1998; 98US-0021141.  
PR 08-NOV-1998; 98US-00184216.  
PR 08-NOV-1998; 98US-00187368.  
PR 20-DEC-1998; 98US-00202054.  
PR 20-DEC-1998; 98US-00218517.  
PR 05-JAN-1999; 99US-00000106.  
PR 05-MAR-1999; 99US-00254465.  
PR 08-MAR-1999; 99US-00005028.  
PR 10-MAR-1999; 99US-00265686.  
PR 10-MAR-1999; 99US-00005190.  
PR 12-APR-1999; 99US-00284291.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99US-00107033.  
PR 02-JUN-1999; 99US-00101252.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380142.  
PR 30-NOV-1999; 99US-00283113.  
PR 02-DEC-1999; 99US-00285511.  
PR 02-DEC-1999; 99US-00285655.  
PR 16-DEC-1999; 99US-00300095.  
PR 30-DEC-1999; 99US-00311243.  
PR 30-DEC-1999; 99US-00311274.  
PR 05-JAN-2000; 2000US-0000219.  
PR 06-JAN-2000; 2000US-0000277.  
PR 06-JAN-2000; 2000US-0000376.  
PR 11-FEB-2000; 2000US-0003565.  
PR 18-FEB-2000; 2000US-0004341.  
PR 24-FEB-2000; 2000US-0005004.  
PR 24-FEB-2000; 2000US-0005941.  
PR 10-MAR-2000; 2000US-0006319.  
PR 21-MAR-2000; 2000US-0007532.  
PR 30-MAR-2000; 2000US-0008439.  
PR 17-MAY-2000; 2000US-0013705.  
PR 22-MAY-2000; 2000US-0014042.  
PR 30-MAY-2000; 2000US-0014941.  
PR 02-JUN-2000; 2000US-0015264.  
PR 28-JUL-2000; 2000US-0020710.  
PR 24-AUG-2000; 2000US-0023328.  
PR 08-NOV-2000; 2000US-00709238.  
PR 27-NOV-2000; 2000US-00723749.  
PR 01-DEC-2000; 2000US-0032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 28-FEB-2001; 2000US-0034956.  
PR 28-FEB-2001; 2001US-0006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 22-MAR-2001; 2001US-00816920.  
PR 22-MAR-2001; 2001US-0009552.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-0017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001US-00871780.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001US-0019692.  
PR 29-JUN-2001; 2001US-0021066.  
PR 09-JUL-2001; 2001US-0021735.  
PR 30-JUL-2001; 2001US-00918585.  
XX (GETH ) GENENTECH INC.  
XX Askenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D,  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME,  
PI Goddard A, Godowski P, Grimaldi JC, Gurney AL, Hillan KJ,  
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,  
PI Stewart TA, Tumas D, Williams PM, Wood WI,  
XX WPI; 2003-288163/28.  
DR N-PSDB; ABX92267.  
XX Novel secreted and transmembrane polypeptides and polynucleotides  
PT encoding them useful for treating cancer, kidney diseases, bone,  
PT cartilage disorders and immune deficiencies.  
XX Claim 12; Fig 4; 459pp; English.  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for  
CC identifying agonists or antagonists. The bioactive molecule maybe a  
CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.  
CC The PRO polypeptides are useful for treating immune disorders, diabetes  
CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system  
CC disorders, kidney disorders, bone and cartilage disorders or arthritis,  
CC tumours, and wound healing. The polynucleotide sequences encoding PRO  
CC polypeptides are useful as hybridisation probes, in chromosome and gene  
CC mapping, in the generation of antisense RNA and DNA, in the preparation  
CC of PRO polypeptides, for generating transgenic animals or knockout  
CC animals, for the genetic analysis of individuals with genetic disorders,  
CC and in gene therapy. AB061071-AB061164 represent the human PRO  
CC polypeptides of the invention. Note: The sequence data for this patent  
CC was obtained in electronic format directly from the USPTO web site at  
CC seqdata.uspto.gov/psipsdEntry.html  
XX  
SQ Sequence 492 AA;  
Query Match 100.0%; Score 2527; DB 6; Length 492;  
Best Local Similarity 100.0%; Pred. No. 1.4e-285;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MVKFPALTHYWLIRFLVPLGTTITAIIDFGQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
DB 1 MVKFPALTHYWLIRFLVPLGTTITAIIDFGQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
QY 61 FFTGPMSPFNKVLGVFVNSKRDRTKAVLCWVAGAAVFTHTLIAYSDLYGYYINKLHHV 120  
DB 61 FFTGPMSPFNKVLGVFVNSKRDRTKAVLCWVAGAAVFTHTLIAYSDLYGYYINKLHHV 120  
QY 121 DESVGSKTRAPLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAIL 180  
DB 121 DESVGSKTRAPLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAIL 180  
QY 181 HSHLECREPLIPILSLYMGALVRCITLCLGYKNIHDIIPDRSGPELGDDATIRMLSF 240  
DB 181 HSHLECREPLIPILSLYMGALVRCITLCLGYKNIHDIIPDRSGPELGDDATIRMLSF 240  
QY 241 WNPALILATQIRISRPVNLFSRDLGGSSAATEAVAILTATPYGHPYGLWLTIRAVY 300  
DB 241 WNPALILATQIRISRPVNLFSRDLGGSSAATEAVAILTATPYGHPYGLWLTIRAVY 300  
QY 301 PAFDKNPNKLVSTNTVTAHKKFTVCNALSITLCFVNFMTFNPVNSEKILIDIIIGVD 360  
DB 301 PAFDKNPNKLVSTNTVTAHKKFTVCNALSITLCFVNFMTFNPVNSEKILIDIIIGVD 360

QY 361 FAFAPLGVPIRISFFPVPVTRAHLTGWMLTKTFLVAPSVLRIRIIVLIASLVLPY 420  
DB 361 FAFAPLGVPIRISFFPVPVTRAHLTGWMLTKTFLVAPSVLRIRIIVLIASLVLPY 420  
QY 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRQKKWENESATEGEDSANTDMPTEE 480  
DB 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRQKKWENESATEGEDSANTDMPTEE 480  
QY 481 VTDIVEMRENE 492  
DB 481 VTDIVEMRENE 492  
RESULT 8  
ID ABU80341 standard; protein; 492 AA.  
XX AC ABU80341;  
XX DT 24-JUN-2003 (first entry)  
XX DE Human secreted/transmembrane protein PRO274.  
XX KW Human; secreted protein; transmembrane protein; PRO; malignancy; cancer;  
KW ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma;  
KW inflammatory disease; necrosis; atherosclerosis; infertility;  
KW premature aging; psoriasis; inflammatory disease; renal disease;  
KW arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis;  
KW multiple sclerosis; gene therapy.  
XX OS Homo sapiens.  
XX PN US2003004102-A1.  
XX PD 02-JAN-2003.  
XX PF 15-OCT-2001; 2001US-00978189.  
XX PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 13-MAR-1998; 98US-0077791P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078862P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 26-JUN-1998; 98US-00105413.  
PR 07-OCT-1998; 98US-00168978.  
PR 07-OCT-1998; 98US-00211141.  
PR 02-NOV-1998; 98US-00184216.  
PR 06-NOV-1998; 98US-00187368.  
PR 20-NOV-1998; 98US-00204855.  
PR 07-DEC-1998; 98US-00202054.  
PR 30-DEC-1998; 98US-00218517.  
PR 05-JAN-1999; 99US-00000106.  
PR 03-MAR-1999; 99US-00254465.

99WO-US005028.  
99US-00255686.  
99WO-US005159.  
99US-00257213.  
99US-00284291.  
99US-00311832.  
99WO-US010733.  
99WO-US012252.  
99US-00380137.  
99US-00380138.  
99US-00380142.  
99WO-US028313.  
99WO-US028551.  
99WO-US028565.  
99WO-US030095.  
99WO-US031243.  
99WO-US031274.  
2000WO-US000219.  
2000WO-US000277.  
2000WO-US000376.  
2000WO-US003565.  
2000WO-US004341.  
2000WO-US005004.  
2000WO-US005601.  
2000WO-US005841.  
2000WO-US006319.  
2000WO-US007532.  
2000WO-US008439.  
2000WO-US013705.  
2000WO-US014042.  
2000WO-US014941.  
2000WO-US015264.  
2000WO-US020710.  
2000WO-US023328.  
2000US-00709238.  
2000WO-US030873.  
2000US-00723749.  
2000WO-US032678.  
2000US-00747259.  
2000WO-US034956.  
2000WO-US006520.  
2001US-00816744.  
2001US-00816920.  
2001WO-US009552.  
2001US-00854208.  
2001US-00854280.  
2001WO-US017092.  
2001US-00872035.  
2001WO-US017800.  
2001US-00874503.  
2001US-00882636.  
2001US-00886342.  
2001US-00891992.  
2001WO-US021066.  
2001WO-US021735.  
2001US-00918585.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Borstein D, Deanoyers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME;  
PI Goddard A, Godowski Fu, Grimaldi JC, Gurney AL, Hillan KJ,  
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PM, Wood WI;  
XX WPI; 2003-341189/32.  
XX N-PSDB; ACA66008.  
XX New genes and secreted and transmembrane polypeptides (e.g. PRO337 or  
PT PRO1559), useful for treating or diagnosing e.g. cancers,  
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple  
PT sclerosis in mammals.

Claim 12; Fig 4; 460pp; English.

Claim 12; Fig 4; 460pp; English.

The invention relates to a new isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of 94 PRO polypeptides whose sequences are fully defined in the specification; or (b) any of 94 nucleotide sequences fully defined in the specification; or the full length coding sequence of any these 94 nucleotide sequences. Also included are an isolated PRO polypeptide scoring at least 80% positives when compared to any of the PRO polypeptide sequences cited above (or an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) an amino acid sequence encoded by the nucleotide deposited with ATCC numbers listed in the specification; (b) the PRO polypeptide, lacking its associated signal peptide; or (c) an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide), a vector comprising the nucleic acid molecule, a host cell comprising the vector (and producing a PRO polypeptide), a chimeric molecule comprising the PRO polypeptide fused to a heterologous amino acid sequence and an anti-PRO antibody. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioeffectors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease, necrosis, atherosclerosis, infertility, premature aging, psoriasis, inflammatory disease, renal disease, arthritis, immune-mediated alopecia, stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a PRO polypeptide

Sequence 492 AA;

Query Match	100.0%;	Score 2527;	DB 6;	Length 492;
Best Local Similarity	100.0%;	Pred. No. 1.4e-285;		
Matches 492;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MVKFPALTHYWPILRFLVPLGTITIAIDFGQALNRGIAA	KEDAVEMLASVGLAYSLMK	60
Db	1	MVKFPALTHYWPILRFLVPLGTITIAIDFGQALNRGIAA	KEDAVEMLASVGLAYSLMK	60
QY	61	FTGPMSPFKNVGLVFNNSKEDRDKAVLCWVAGAAIAA	VFHTLLIAYSDILGYIINKLHV	120
Db	61	FTGPMSPFKNVGLVFNNSKEDRDKAVLCWVAGAAIAA	VFHTLLIAYSDILGYIINKLHV	120
QY	121	DESVGSKTRRAFLYLAAAPFFPDAMANTHAGILLKHKTS	FLVGCASISDVIAQVVFVAILL	180
Db	121	DESVGSKTERAFLYLAAAPFFPDAMANTHAGILLKHKYS	FLVGCASISDVIAQVVFVAILL	180
QY	181	HSHLECREPELLIPILUSLWYALVRCCTLCIGYYKNIHDI	IPDRSGPELGGDATIRKMLSF	240
Db	181	HSHLECREPELLIPILUSLWYALVRCCTLCIGYYKNIHDI	IPDRSGPELGGDATIRKMLSF	240
QY	241	WWPALLILATQIRISRPINVLVFSRDLGSSSAATEA	VAAILTATVPVGHMPPYGLWLTIRAVY	300
Db	241	WWPALLILATQIRISRPINVLVFSRDLGSSSAATEA	VAAILTATVPVGHMPPYGLWLTIRAVY	300
QY	301	PAFDKNNPSKNLVSTNTVTAAHIKKFTFCWMLSLTLC	FCWMPWPNVSEKILIDIGVD	360
Db	301	PAFDKNNPSKNLVSTNTVTAAHIKKFTFCWMLSLTLC	FCWMPWPNVSEKILIDIGVD	360
QY	361	FAPAELCVVPLRIFSGFFPVPTVRAHLTGWLMTLTKT	FVLAPSSVLRILVLIASLVLPY	420
Db	361	FAPAELCVVPLRIFSGFFPVPTVRAHLTGWLMTLTKT	FVLAPSSVLRILVLIASLVLPY	420
QY	421	LGVHGNLTGVGSLLAGFVGSEMTWAAIAACYVYRKQ	KKMMENESATEGDSAMTDMPTTEE	480
Db	421	LGVHGNLTGVGSLLAGFVGSEMTWAAIAACYVYRKQ	KKMMENESATEGDSAMTDMPTTEE	480
QY	481	VTDIVEMRENE	492	

Db	481	VTDIVEMRENE	492
RESULT 9			
ADA24546			
ID	ADA24546	standard; protein; 492 AA.	
XX	XX		
AC	ADA24546;		
XX			
XX	20-NOV-2003	(first entry)	
XX			
DE	Novel human secreted and transmembrane protein	PRO274.	
XX			
XX	Human; secreted and transmembrane protein; PRO; tissue		
KW	Chromosome identification; vaccine; cancer; retinal dis		
KW	sports-related joint disorder; osteoarthritis; rheumat		
KW	wound healing; obesity; diabetes; hearing loss;		
KW	cardiac insufficiency disorder; kidney disorder; nervo		
KW	haemoglobin associated disorder.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003050241-A1.		
XX			
PD	13-MAR-2003.		
XX			
PF	16-OCT-2001; 2001US-00978564.		
XX			
PR	17-OCT-1997; 97US-0062250P.		
PR	03-NOV-1997; 97US-0064249P.		
PR	13-NOV-1997; 97US-0065311P.		
PR	21-NOV-1997; 97US-0066364P.		
PR	10-MAR-1998; 98US-0077450P.		
PR	11-MAR-1998; 98US-0077632P.		
PR	11-MAR-1998; 98US-0077641P.		
PR	11-MAR-1998; 98US-0077649P.		
PR	12-MAR-1998; 98US-0077791P.		
PR	13-MAR-1998; 98US-0078004P.		
PR	20-MAR-1998; 98US-0078086P.		
PR	20-MAR-1998; 98US-0078910P.		
PR	20-MAR-1998; 98US-0078936P.		
PR	20-MAR-1998; 98US-0078939P.		
PR	26-MAR-1998; 98US-0079234P.		
PR	26-MAR-1998; 98US-0079656P.		
PR	27-MAR-1998; 98US-0079663P.		
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PR	27-MAR-1998; 98US-0079689P.		
PR	27-MAR-1998; 98US-0079728P.		
PR	27-MAR-1998; 98US-0079786P.		
PR	30-MAR-1998; 98US-0079920P.		
PR	30-MAR-1998; 98US-0079923P.		
PR	31-MAR-1998; 98US-0080105P.		
PR	31-MAR-1998; 98US-0080107P.		
PR	31-MAR-1998; 98US-0080165P.		
PR	31-MAR-1998; 98US-0080194P.		
PR	01-APR-1998; 98US-0080327P.		
PR	01-APR-1998; 98US-0080328P.		
PR	01-APR-1998; 98US-0080333P.		
PR	01-APR-1998; 98US-0080334P.		
PR	08-APR-1998; 98US-0081049P.		
PR	08-APR-1998; 98US-0081070P.		
PR	08-APR-1998; 98US-0081071P.		
PR	09-APR-1998; 98US-0081195P.		
PR	09-APR-1998; 98US-0081203P.		
PR	09-APR-1998; 98US-0081229P.		
PR	15-APR-1998; 98US-0081817P.		
PR	15-APR-1998; 98US-0081819P.		
PR	15-APR-1998; 98US-0081838P.		
PR	15-APR-1998; 98US-0081952P.		
PR	15-APR-1998; 98US-0081955P.		
PR	21-APR-1998; 98US-0082568P.		
PR	21-APR-1998; 98US-0082569P.		

PR	22-APR-1998;	98US-008700P.
PR	22-APR-1998;	98US-008704P.
PR	22-APR-1998;	98US-008797F.
PR	22-APR-1998;	98US-008804P.
PR	23-APR-1998;	98US-008796F.
PR	23-APR-1998;	98US-008336P.
PR	27-APR-1998;	98US-008332P.
PR	29-APR-1998;	98US-008392P.
PR	29-APR-1998;	98US-008349SP.
PR	29-APR-1998;	98US-008349FP.
PR	29-APR-1998;	98US-008349PP.
PR	29-APR-1998;	98US-0083500P.
PR	29-APR-1998;	98US-008354SP.
PR	29-APR-1998;	98US-008355P.
PR	29-APR-1998;	98US-008355B.
PR	29-APR-1998;	98US-008355BP.
PR	30-APR-1998;	98US-0083742P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	07-MAY-1998;	98US-008459B.
PR	07-MAY-1998;	98US-0084600P.
PR	07-MAY-1998;	98US-0084627P.
PR	07-MAY-1998;	98US-0084637P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	13-MAY-1998;	98US-0085323P.
PR	13-MAY-1998;	98US-0085338P.
PR	13-MAY-1998;	98US-0085339P.
PR	15-MAY-1998;	98US-0085573P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085689P.
PR	15-MAY-1998;	98US-0085697P.
PR	15-MAY-1998;	98US-008700P.
PR	15-MAY-1998;	98US-008704P.
PR	18-MAY-1998;	98US-0086023P.
PR	22-MAY-1998;	98US-0086392P.
PR	22-MAY-1998;	98US-0086414P.
PR	22-MAY-1998;	98US-0086430P.
PR	22-MAY-1998;	98US-0086466P.
PR	28-MAY-1998;	98US-0087098P.
PR	28-MAY-1998;	98US-0087106P.
PR	28-MAY-1998;	98US-0087208P.
PR	28-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	30-JUL-1998;	98US-0094651P.
PR	11-SEP-1998;	98US-0100038P.
PR	07-OCT-1998;	98WO-US021141.
PR	20-NOV-1998;	98WO-US019304P.
PR	20-NOV-1998;	98WO-US024855.
PR	22-DEC-1998;	98US-0113396P.
PR	23-DEC-1998;	98US-0113421P.
PR	03-JAN-1999;	99WO-US000106.
PR	08-MAR-1999;	99WO-US005028.
PR	10-MAR-1999;	99WO-US005190.
PR	12-MAR-1999;	99US-0123957P.
PR	29-MAR-1999;	99US-0126773P.
PR	21-APR-1999;	99US-0130323P.
PR	26-APR-1999;	99US-0131022P.
PR	28-APR-1999;	99US-0131445P.
PR	14-MAY-1999;	99US-0134287P.
PR	14-MAY-1999;	99WO-US010733.
PR	02-JUN-1999;	99WO-US012252.
PR	16-JUN-1999;	99US-0139557P.
PR	23-JUN-1999;	99US-0141037P.
PR	07-JUL-1999;	99US-0142680P.
PR	26-JUL-1999;	99US-0145698P.
PR	28-JUL-1999;	99US-0146222P.
PR	29-OCT-1999;	99US-0162506P.
PR	30-NOV-1999;	99WO-US028313.
PR	02-DEC-1999;	99WO-US028551.
PR	16-DEC-1999;	99WO-US028565.
PR	30-DEC-1999;	99WO-US030095.
PR	30-DEC-1999;	99WO-US031243.
PR	30-DEC-1999;	99WO-US031274.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000277.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	21-MAR-2000;	2000WO-US007532.
PR	30-MAR-2000;	2000WO-US008439.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	28-JUL-2000;	2000WO-US020710.
PR	24-AUG-2000;	2000WO-US023328.
PR	01-DEC-2000;	2000WO-US032678.
PR	28-DEC-2000;	2000WO-US034956.
PR	28-FEB-2001;	2001WO-US006520.
PR	22-MAR-2001;	2001WO-US009552.
PR	25-MAY-2001;	2001WO-US017092.
PR	01-JUN-2001;	2001WO-US017800.
PR	20-J	



QY 121 DESVGSKTRAFILYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVFWVAILL 180  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
Db 121 DESVGSKTRAFILYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVFWVAILL 180  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
QY 181 HSHLECREPELLIPILSYNGALVRCITLCLGYGKNIHDIIPRSGPELGGDATIRKMLSF 240  
PR 31-MAR-1998; 98US-0080105P.  
PR 31-MAR-1998; 98US-0080107P.  
Db 181 HSHLECREPELLIPILSYNGALVRCITLCLGYGKNIHDIIPRSGPELGGDATIRKMLSF 240  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
QY 241 WMLALILATORISRIIVNLFVSRDLGGSSAAATEAVAILTATYPVGHMPYGNLTIRAVY 300  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
Db 241 WMLALILATORISRIIVNLFVSRDLGGSSAAATEAVAILTATYPVGHMPYGNLTIRAVY 300  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
QY 301 PAFDKNPNKLVSTNTVTAHKFTFCVWALSITLCLFVWFVNTNSEKILIDIIIGVD 360  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
Db 301 PAFDKNPNKLVSTNTVTAHKFTFCVWALSITLCLFVWFVNTNSEKILIDIIIGVD 360  
PR 08-APR-1998; 98US-0081071P.  
PR 08-APR-1998; 98US-0081195P.  
QY 361 FAFAEICVWPLRIFSFPPVPTVRAHLTGWMLTKKTFVLAPSSVLRILIVLIASLWVLPY 420  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
Db 361 FAFAEICVWPLRIFSFPPVPTVRAHLTGWMLTKKTFVLAPSSVLRILIVLIASLWVLPY 420  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081819P.  
QY 421 LGVHGATLGVGSLLAGFVGEESTVVAIAACVYVRKQKKMENESATEGDSAMTDPPTTE 480  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081922P.  
Db 421 LGVHGATLGVGSLLAGFVGEESTVVAIAACVYVRKQKKMENESATEGDSAMTDPPTTE 480  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
QY 481 VTDIVENRENE 492  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
Db 481 VTDIVENRENE 492  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
QY 481 VTDIVENRENE 492  
PR 22-APR-1998; 98US-0082804P.  
PR 22-APR-1998; 98US-0082796P.  
PR 23-APR-1998; 98US-0083336P.  
PR 27-APR-1998; 98US-0083332P.  
QY 08-SEP-2003 (first entry)  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083498P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084441P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085577P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 26-JUN-1998; 98US-0091010P.  
RESULT 10  
ABO19643  
ID ABO19643 standard; protein; 492 AA.  
XX AC ABO19643;  
XX DT  
XX DE Novel human secreted and transmembrane protein PRO274.  
XX KW Human; secreted and transmembrane protein; PRO; cell death; neuropathy;  
XX KW peripheral neuropathy; diabetic peripheral neuropathy;  
XX KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;  
XX KW Refsum's disease; Abetalipoproteinemia; Tangier disease;  
XX KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;  
XX KW Dejerine-Sottas syndrome; chromosome mapping; gene mapping; gene therapy.  
OS Homo sapiens.  
XX US2003050240-A1.  
XX PD 13-MAR-2003.  
XX PF 16-OCT-2001; 2001US-00978403.  
XX PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 20-MAR-1998; 98US-0078866P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079565P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.

PR	01-JUL-1998;	98US-0091359P.	PS	Claim 12; Fig 4; 459pp; English.
PR	30-JUL-1998;	98US-0094651P.	XX	The invention describes an isolated, secreted and transmembrane
PR	11-SEP-1998;	98US-0100038P.	CC	polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
PR	07-OCT-1998;	98WO-US021141.	CC	PRO4993, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
PR	20-NOV-1998;	98US-0109304P.	CC	linking a bioactive molecule to a cell expressing the above polypeptides.
PR	20-NOV-1998;	98WO-US024855.	CC	The bioactive molecule is a toxin, radiolabel or an antibody and causes
PR	22-DEC-1998;	98WO-US03296P.	CC	cell death. (I) is useful as therapeutic agent, in medical and industrial
PR	23-DEC-1998;	98US-0113621P.	CC	applications e.g. for treating neuropathy, especially peripheral
PR	05-JAN-1999;	99WO-US000106.	CC	neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
PR	08-MAR-1999;	99WO-US005028.	CC	Charcot-Marie-Tooth disease, Refsum's disease, Abetalipoproteinemia,
PR	10-MAR-1999;	99WO-US005190.	CC	Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's
PR	12-MAR-1999;	99US-01123957P.		
PR	29-MAR-1999;	99US-0126773P.		
PR	21-APR-1999;	99US-0130233P.		
PR	26-APR-1999;	99US-0131022P.		
PR	28-APR-1999;	99US-0131445P.		
PR	14-MAY-1999;	99US-01342073.		
PR	02-JUN-1999;	99WO-US012252.		
PR	16-JUN-1999;	99US-0135557P.		
PR	23-JUN-1999;	99US-0141037P.		
PR	07-JUL-1999;	99US-0142680P.		
PR	26-JUL-1999;	99US-0145698P.		
PR	28-JUL-1999;	99US-0146222P.		
PR	29-OCT-1999;	99US-0162506P.		
PR	30-NOV-1999;	99WO-US028313.		
PR	02-DEC-1999;	99WO-US028551.		
PR	02-DEC-1999;	99WO-US028565.		
PR	16-DEC-1999;	99WO-US030095.		
PR	30-DEC-1999;	99WO-US031243.		
PR	05-JAN-2000;	2000WO-US000219.		
PR	06-JAN-2000;	2000WO-US000277.		
PR	06-JAN-2000;	2000WO-US000376.		
PR	11-FEB-2000;	2000WO-US003565.		
PR	18-FEB-2000;	2000WO-US004341.		
PR	24-FEB-2000;	2000WO-US005004.		
PR	02-MAR-2000;	2000WO-US005841.		
PR	10-MAR-2000;	2000WO-US006319.		
PR	21-MAR-2000;	2000WO-US007532.		
PR	30-MAR-2000;	2000WO-US008439.		
PR	17-MAY-2000;	2000WO-US013705.		
PR	22-MAY-2000;	2000WO-US014042.		
PR	30-MAY-2000;	2000WO-US014941.		
PR	02-JUN-2000;	2000WO-US015264.		
PR	28-JUL-2000;	2000WO-US020710.		
PR	24-AUG-2000;	2000WO-US023328.		
PR	01-DEC-2000;	2000WO-US032678.		
PR	20-DEC-2000;	2000WO-US034956.		
PR	28-FEB-2001;	2001WO-US006520.		
PR	22-MAR-2001;	2001WO-US009552.		
PR	25-MAY-2001;	2001WO-US017092.		
PR	01-JUN-2001;	2001WO-US017800.		
PR	20-JUN-2001;	2001WO-US019692.		
PR	29-JUN-2001;	2001WO-US021066.		
PR	09-JUL-2001;	2001WO-US021735.		
PR	30-JUL-2001;	2001US-00918585.		
XX	(GETH ) GENENTECH INC.			
XX	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;			
XX	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;			
PI	Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;			
PI	Kljarin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;			
PI	Stewart TA, Tumas D, Williams PM, Wood WL;			
XX	WPI; 2003-503575/47.			
DR	N-PSDB; ACD29609.			
XX	Novel secreted and transmembrane polypeptide for modulating biological			
XX	activity of cell expressing the polypeptide, identifying agonists or			
PT	antagonists of polypeptide, and as molecular weight markers.			
XX				

QY	1	MVKFPALTYWPLIRFLVPLGITNTAIDFGEOALNRGIAA VKEDAVEMLASGLAYSLMK	60
Db	1	MVKFPALTYWPLIRFLVPLGITNTAIDFGEOALNRGIAA VKEDAVEMLASGLAYSLMK	60
QY	61	FTGPMSEKNGVGLVFNVSKRDRTKAVLCMVVAGAAV FHTLIAYSDLGYYIINKLHV	120
Db	61	FTGPMSEKNGVGLVFNVSKRDRTKAVLCMVVAGAAV FHTLIAYSDLGYYIINKLHV	120
QY	121	DESVGSKTRRAFLYLAAPFFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQWVFVAILL	180
Db	121	DESVGSKTRRAFLYLAAPFFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQWVFVAILL	180
QY	181	HSHECREPLILSLYMGALVRCITTLCLGYVKNHDIIPRSGPELGGDATIRKMLSF	240
Db	181	HSHECREPLILSLYMGALVRCITTLCLGYVKNHDIIPRSGPELGGDATIRKMLSF	240
QY	241	WWPLALILATQIRISRPVNLVSRDLGGSSAATEAVAILTATYPVGHMPYGMLEIRAVY	300
Db	241	WWPLALILATQIRISRPVNLVSRDLGGSSAATEAVAILTATYPVGHMPYGMLEIRAVY	300
QY	301	PAFDKKNPSNKLIVSTNTVTAHKKFTFVCVWALSITLCFVWFTEVNSEKILIDIIIGVD	360
Db	301	PAFDKKNPSNKLIVSTNTVTAHKKFTFVCVWALSITLCFVWFTEVNSEKILIDIIIGVD	360
QY	361	FAPAECLVVPRLIFSPFPVTVRAHLTGWMLTKKTFVLAPSSVLRIIVLIASLVLPY	420
Db	361	FAPAECLVVPRLIFSPFPVTVRAHLTGWMLTKKTFVLAPSSVLRIIVLIASLVLPY	420
QY	421	LGVHGATLGVGSLLAGFVGESTWVAIAACVYVKQKKMENESATGEDSAMTDPTEE	480
Db	421	LGVHGATLGVGSLLAGFVGESTWVAIAACVYVKQKKMENESATGEDSAMTDPTEE	480
QY	481	VTDIVENRENE	492
Db	481	VTDIVENRENE	492
RESULT 11			
ADAL2207			
ID	ADAL2207 standard; protein; 492 AA.		
XX	ADAL2207;		
AC	ADAL2207;		
XX	06-NOV-2003 (first entry)		
DT	Human secreted/transmembrane polypeptide PRO274.		
DE	inflammatory disease; organ failure; atherosclerosis; cardiac injury;		
XX	infertility; birth defect; premature aging; AIDS; cancer;		
KW	diabetic complication; tissue typing; human.		
XX	Homo sapiens.		
OS	US2003055216-A1.		
XX	20-WAR-2003.		
PN			
XX			
XX			
PT			
XX			

XX 17-OCT-2001; 2001US-00978824.  
XX 21-MAY-1996; 96US-0018049P.  
XX 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077841P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 22-MAR-1998; 98US-0079294P.  
PR 25-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 27-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 31-MAR-1998; 98US-0080105P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081819P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081922P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 22-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082797P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 29-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
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PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084444P.  
PR 06-MAY-1998; 98US-0084441P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084633P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085339P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085589P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 15-MAY-1998; 98US-0085704P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 22-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 26-JUN-1998; 98US-00105413.  
PR 26-JUN-1998; 98US-0090863P.  
PR 26-JUN-1998; 98US-0091010P.  
PR 01-JUL-1998; 98US-0091359P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.  
PR 07-OCT-1998; 98US-00168978.  
PR 07-OCT-1998; 98WO-US021141.  
PR 02-NOV-1998; 98US-00184216.  
PR 06-NOV-1998; 98US-00187368.  
PR 20-NOV-1998; 98US-0109304P.  
PR 20-NOV-1998; 98WO-US024855.  
PR 07-DEC-1998; 98US-00202054.  
PR 22-DEC-1998; 98US-00218517.  
PR 22-DEC-1998; 98US-0113296P.  
PR 23-DEC-1998; 98US-0113621P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 05-MAR-1999; 99US-00254465.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99US-00285686.  
PR 10-MAR-1999; 99WO-US005190.  
PR 12-MAR-1999; 99US-00267213.  
PR 12-MAR-1999; 99US-0123957P.  
PR 29-MAR-1999; 99US-0126773P.  
PR 12-APR-1999; 98US-00284291.  
PR 21-APR-1999; 98US-0130232P.  
PR 26-APR-1999; 98US-0131022P.  
PR 28-APR-1999; 98US-0131145P.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 14-MAY-1999; 99WO-US012252.  
PR 16-JUN-1999; 98US-0139557P.  
PR 23-JUN-1999; 98US-0141037P.  
PR 07-JUL-1999; 98US-0142680P.  
PR 26-JUL-1999; 98US-0145698P.  
PR 28-JUL-1999; 98US-0146222P.  
PR 25-AUG-1999; 98US-00380137.  
PR 25-AUG-1999; 98US-00380138.  
PR 25-AUG-1999; 98US-00380142.  
PR 29-OCT-1999; 98US-0162506P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.

PR	24-FEB-2000;	200WO-US005004.
PR	02-MAR-2000;	200WO-US005841.
PR	10-MAR-2000;	200WO-US006319.
PR	21-MAR-2000;	200WO-US007532.
PR	30-MAR-2000;	200WO-US008439.
PR	17-MAY-2000;	200WO-US013705.
PR	22-MAY-2000;	200WO-US014042.
PR	30-MAY-2000;	200WO-US014941.
PR	02-JUN-2000;	200WO-US015264.
PR	28-JUL-2000;	200WO-US020710.
PR	24-AUG-2000;	200WO-US023328.
PR	08-NOV-2000;	200US-00709238.
PR	27-NOV-2000;	200US-00723749.
PR	01-DEC-2000;	200WO-US032678.
PR	20-DEC-2000;	200US-00747259.
PR	20-DEC-2000;	200WO-US034956.
PR	28-FEB-2001;	200WO-US006520.
PR	22-MAR-2001;	200US-00816744.
PR	22-MAR-2001;	200US-00816920.
PR	22-MAR-2001;	200WO-US009552.
PR	10-MAY-2001;	200US-00854288.
PR	10-MAY-2001;	200US-00854280.
PR	21-MAY-2001;	200WO-US017092.
PR	01-JUN-2001;	200US-00872035.
PR	01-JUN-2001;	200WO-US017800.
PR	05-JUN-2001;	200US-00874503.
PR	14-JUN-2001;	200US-00882636.
PR	19-JUN-2001;	200US-00886342.
PR	20-JUN-2001;	200WO-US019692.
PR	29-JUN-2001;	200WO-US021066.
PR	09-JUL-2001;	200WO-US021735.
PR	30-JUL-2001;	200US-00918585.
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Ashtenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;	
PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;	

Query Match

Best Local Similarity 100.0%; Score 2527; DB 6; Length 492;

Mismatches 0; Conservative 0; Indels 0; Gaps 0;

QY	1	MVKFPALHYWLLRFLVPLGLTNTAIDFGEQALNRTAAVKEDAVEMLASGLAYSIMK	60
DB	1	MVKFPALHYWLLRFLVPLGLTNTAIDFGEQALNRTAAVKEDAVEMLASGLAYSIMK	60
QY	61	FTGPMSPDKVGLVFNVSKRDTKAVLCWVAGAAVAFHTLIAYSDLGYYIINKLHV	120
DB	61	FTGPMSPDKVGLVFNVSKRDTKAVLCWVAGAAVAFHTLIAYSDLGYYIINKLHV	120
QY	121	DESVGSKTRAFILYLAAPFMDAMAWTHAGIILKHYSFLVGCASISDVIAQVFWAILL	180
DB	121	DESVGSKTRAFILYLAAPFMDAMAWTHAGIILKHYSFLVGCASISDVIAQVFWAILL	180
QY	181	HSLECREPLILPILSYMGALVRCCTLCGLYKNIHDIIPDRSGPELGGDATIRKMLSF	240
DB	181	HSLECREPLILPILSYMGALVRCCTLCGLYKNIHDIIPDRSGPELGGDATIRKMLSF	240
QY	241	WWPLALILATORISRPVNLFSRDLGSSAATEAVAILTATYPVGHMPYGMTIRAVY	300
DB	241	WWPLALILATORISRPVNLFSRDLGSSAATEAVAILTATYPVGHMPYGMTIRAVY	300
QY	301	PAFDKNPSKNLYSTNTVTAHKKFTFVCMAISLTLFCVFWFTNVSEKILIDIIQVD	360
DB	301	PAFDKNPSKNLYSTNTVTAHKKFTFVCMAISLTLFCVFWFTNVSEKILIDIIQVD	360
QY	361	FAFAELCWVPLRIFSPFPVTVRAHLTGWMLTKKTFVLAPSSVLRIIVLIASIVLDPY	420
DB	361	FAFAELCWVPLRIFSPFPVTVRAHLTGWMLTKKTFVLAPSSVLRIIVLIASIVLDPY	420
QY	421	LGVHGATLGVGSILLAGFVGSMTVAACVYVKOKKMNESATGEDSAMDTPPTEE	480
DB	421	LGVHGATLGVGSILLAGFVGSMTVAACVYVKOKKMNESATGEDSAMDTPPTEE	480

QY	481	VTDIVMEENE 492
DB	481	VTDIVMEENE 492
RESULT 12		
ABO19534		
ID	ABO19534	standard; protein; 492 AA.
XX		
AC	ABO19534;	
XX		
DT	27-AUG-2003	(first entry)
XX		
DE		Novel human secreted and transmembrane polypeptide #2.
XX		
KW		Human; secreted and transmembrane protein; PRO; viral infection;
KW		tumour growth; retinal disorder; injury; sight loss;
KW		retinitis pigmentosa; age-related macular degeneration;
KW		sport-related joint problem; articular cartilage defect; osteoarthritis;
KW		rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
KW		kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW		celiac disease; dermatitis; Crohn disease; neuropathy;
KW		cardiac insufficiency disorder; peripheral neuropathy;
KW		diabetic peripheral neuropathy; autonomic neuropathy;
KW		reduced motility of the gastrointestinal tract;
KW		atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW		Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW		Refsum's disease.
XX		
OS		Homo sapiens.
XX		
PN		US2003049633-A1.
XX		
PD		13-MAR-2003.
XX		
PF		16-OCT-2001; 2001US-00978585.
XX		
PR	17-OCT-1997;	97US-0062250P.
PR	03-NOV-1997;	97US-0064249P.
PR	13-NOV-1997;	97US-0065311P.
PR	21-NOV-1997;	97US-0066364P.
PR	10-MAR-1998;	98US-0077450P.
PR	11-MAR-1998;	98US-0077632P.
PR	11-MAR-1998;	98US-0077841P.
PR	11-MAR-1998;	98US-0077849P.
PR	12-MAR-1998;	98US-0077791P.
PR	13-MAR-1998;	98US-0078004P.
PR	17-MAR-1998;	98US-00040220.
PR	20-MAR-1998;	98US-0078886P.
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PR	20-MAR-1998;	98US-0078936P.
PR	20-MAR-1998;	98US-0078939P.
PR	25-MAR-1998;	98US-0079294P.
PR	26-MAR-1998;	98US-0079656P.
PR	27-MAR-1998;	98US-0079663P.
PR	27-MAR-1998;	98US-0079664P.
PR	27-MAR-1998;	98US-0079689P.
PR	27-MAR-1998;	98US-0079728P.
PR	27-MAR-1998;	98US-0079786P.
PR	30-MAR-1998;	98US-0079920P.
PR	30-MAR-1998;	98US-0079923P.
PR	31-MAR-1998;	98US-0080105P.
PR	31-MAR-1998;	98US-0080107P.
PR	31-MAR-1998;	98US-0080165P.
PR	31-MAR-1998;	98US-0080194P.
PR	01-APR-1998;	98US-0080327P.
PR	01-APR-1998;	98US-0080328P.
PR	01-APR-1998;	98US-0080333P.
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PR	08-APR-1998;	98US-0081049P.
PR	08-APR-1998;	98US-0081070P.
PR	08-APR-1998;	98US-0081071P.

PR	09-APR-1998;	98US-0081195P.	PR	05-MAR-1999;	99US-00254465.
PR	09-APR-1998;	98US-0081203P.	PR	08-MAR-1999;	99WO-US005028.
PR	09-APR-1998;	98US-0081229P.	PR	10-MAR-1999;	98US-00265686.
PR	15-APR-1998;	98US-0081817P.	PR	10-MAR-1999;	99WO-US005190.
PR	15-APR-1998;	98US-0081819P.	PR	12-MAR-1999;	99US-00267213.
PR	15-APR-1998;	98US-0081838P.	PR	12-MAR-1999;	98US-0123957P.
PR	15-APR-1998;	98US-0081952P.	PR	29-MAR-1999;	99US-0126773P.
PR	15-APR-1998;	98US-0081955P.	PR	12-APR-1999;	99US-00284291.
PR	21-APR-1998;	98US-0082568P.	PR	12-APR-1999;	99US-0130232P.
PR	21-APR-1998;	98US-0082569P.	PR	26-APR-1999;	99US-0131442P.
PR	22-APR-1998;	98US-0082700P.	PR	28-APR-1999;	99US-0131445P.
PR	22-APR-1998;	98US-0082704P.	PR	14-MAY-1999;	99US-00311832.
PR	22-APR-1998;	98US-0082797P.	PR	14-MAY-1999;	99US-0134287P.
PR	22-APR-1998;	98US-0082804P.	PR	14-MAY-1999;	99WO-US010733.
PR	23-APR-1998;	98US-0082796P.	PR	02-JUN-1999;	99US-012252.
PR	23-APR-1998;	98US-0083336P.	PR	16-JUN-1999;	99US-0139557P.
PR	28-APR-1998;	98US-0083332P.	PR	23-JUN-1999;	99US-0141037P.
PR	29-APR-1998;	98US-0083332P.	PR	07-JUL-1999;	99US-0142680P.
PR	29-APR-1998;	98US-0083332P.	PR	26-JUL-1999;	99US-0145698P.
PR	29-APR-1998;	98US-0083495P.	PR	28-JUL-1999;	99US-0146222P.
PR	29-APR-1998;	98US-0083496P.	PR	28-JUL-1999;	99US-00380137.
PR	29-APR-1998;	98US-0083496P.	PR	25-AUG-1999;	99US-00380137.
PR	29-APR-1998;	98US-0083500P.	PR	25-AUG-1999;	99US-00380138.
PR	29-APR-1998;	98US-0083545P.	PR	25-AUG-1999;	99US-00380142.
PR	29-APR-1998;	98US-0083554P.	PR	29-OCT-1999;	99US-0162506P.
PR	29-APR-1998;	98US-0083558P.	PR	30-NOV-1999;	99WO-US028313.
PR	29-APR-1998;	98US-0083559P.	PR	02-DEC-1999;	99WO-US028551.
PR	30-APR-1998;	98US-0083742P.	PR	02-DEC-1999;	99WO-US028565.
PR	06-MAY-1998;	98US-0084142P.	PR	16-DEC-1999;	99WO-US030095.
PR	06-MAY-1998;	98US-0084414P.	PR	30-DEC-1999;	99WO-US031243.
PR	07-MAY-1998;	98US-0084598P.	PR	30-DEC-1999;	99WO-US031274.
PR	07-MAY-1998;	98US-0084600P.	PR	05-JAN-2000;	2000WO-US000219.
PR	07-MAY-1998;	98US-0084627P.	PR	05-JAN-2000;	2000WO-US000277.
PR	07-MAY-1998;	98US-0084637P.	PR	08-JAN-2000;	2000WO-US000376.
PR	07-MAY-1998;	98US-0084639P.	PR	11-FEB-2000;	2000WO-US003565.
PR	07-MAY-1998;	98US-0084640P.	PR	18-FEB-2000;	2000WO-US004341.
PR	07-MAY-1998;	98US-0084643P.	PR	24-FEB-2000;	2000WO-US005004.
PR	13-MAY-1998;	98US-0085323P.	PR	02-MAR-2000;	2000WO-US005841.
PR	13-MAY-1998;	98US-0085338P.	PR	10-MAR-2000;	2000WO-US006319.
PR	13-MAY-1998;	98US-0085339P.	PR	21-MAR-2000;	2000WO-US007532.
PR	15-MAY-1998;	98US-0085573P.	PR	30-MAR-2000;	2000WO-US008439.
PR	15-MAY-1998;	98US-0085579P.	PR	17-MAY-2000;	2000WO-US013705.
PR	15-MAY-1998;	98US-0085580P.	PR	22-MAY-2000;	2000WO-US014042.
PR	15-MAY-1998;	98US-0085582P.	PR	30-MAY-2000;	2000WO-US014941.
PR	15-MAY-1998;	98US-0085689P.	PR	02-JUN-2000;	2000WO-US015264.
PR	15-MAY-1998;	98US-0085697P.	PR	28-JUL-2000;	2000WO-US020710.
PR	15-MAY-1998;	98US-0085700P.	PR	24-AUG-2000;	2000WO-US023328.
PR	15-MAY-1998;	98US-0085704P.	PR	08-NOV-2000;	2000US-00709238.
PR	18-MAY-1998;	98US-0086023P.	PR	27-NOV-2000;	2000US-00723749.
PR	22-MAY-1998;	98US-0086392P.	PR	01-DEC-2000;	2000WO-US032678.
PR	22-MAY-1998;	98US-0086414P.	PR	20-DEC-2000;	2000US-00747259.
PR	22-MAY-1998;	98US-0086430P.	PR	20-DEC-2000;	2000WO-US034956.
PR	22-MAY-1998;	98US-0086486P.	PR	28-FEB-2001;	2001WO-US006520.
PR	28-MAY-1998;	98US-0087098P.	PR	22-MAR-2001;	2001US-00815744.
PR	28-MAY-1998;	98US-0087106P.	PR	22-MAR-2001;	2001US-00818920.
PR	28-MAY-1998;	98US-0087208P.	PR	22-MAR-2001;	2001WO-US009552.
PR	26-JUN-1998;	98US-00105413.	PR	10-MAY-2001;	2001US-00854208.
PR	26-JUN-1998;	98US-0090863P.	PR	10-MAY-2001;	2001US-00854280.
PR	26-JUN-1998;	98US-0091010P.	PR	25-MAY-2001;	2001WO-US017092.
PR	01-JUL-1998;	98US-0093359P.	PR	01-JUN-2001;	2001US-00872035.
PR	11-SEP-1998;	98US-0094651P.	PR	01-JUN-2001;	2001WO-US017800.
PR	07-OCT-1998;	98US-0100038P.	PR	05-JUN-2001;	2001US-00874503.
PR	07-OCT-1998;	98WO-US021141.	PR	14-JUN-2001;	2001US-00882636.
PR	02-NOV-1998;	98US-00184216.			
PR	06-NOV-1998;	98US-00187368.			
PR	20-NOV-1998;	98US-0109304P.			
PR	20-NOV-1998;	98WO-US024855.			
PR	22-DEC-1998;	98US-00202054.			
PR	22-DEC-1998;	98US-00218517.			
PR	23-DEC-1998;	98US-0113296P.			
PR	23-DEC-1998;	98US-0113621P.			
PR	05-JAN-1999;	99WO-US000106.			
			Query Match 100.0%; Score 2527; DB 6; Length 492;		
			Best Local Similarity 100.0%; Pred.No. 1.4e-285;		
			Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MVKFPALTHYWPILRFLVPLGII	1	MVKFPALTHYWPILRFLVPLGII	60
Db	1	MVKFPALTHYWPILRFLVPLGII	1	MVKFPALTHYWPILRFLVPLGII	60
Qy	61	FFTGMSDFKNVGLVFNYSKRDRTKAVLCMVVAGAAAVFHTLIAXSDLGYYIINKLHV	120		

Db 61 FTGPMDFKNGVLFVNSKDRTKAVLCMVVAGAAVPHFTLIAYSDLGYIINKLHV 120  
QY 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGIILKHYSFLVGCASISDVIAQVVFVAILL 180  
D 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGIILKHYSFLVGCASISDVIAQVVFVAILL 180  
QY 181 HSHLECRPELLIPILSLYMGALVRCITICLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240  
D 181 HSHLECRPELLIPILSLYMGALVRCITICLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240  
QY 241 WPLALILATQIRISPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGLWTEIRAVY 300  
D 241 WPLALILATQIRISPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGLWTEIRAVY 300  
QY 301 PAFDKNPSNKLVSNTVTAHHKFTFVCVALSLITLCFVWFMTNPVSEKILDIIGVD 360  
D 301 PAFDKNPSNKLVSNTVTAHHKFTFVCVALSLITLCFVWFMTNPVSEKILDIIGVD 360  
QY 361 PAFALCVVPLRIFFPFVPVTVRAHLTGWMLTKKTFVLAPSSVLRILVLIASLVLPY 420  
D 361 PAFALCVVPLRIFFPFVPVTVRAHLTGWMLTKKTFVLAPSSVLRILVLIASLVLPY 420  
QY 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRKOKKVENESATEGEDSANTDMPPTTE 480  
D 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRKOKKVENESATEGEDSANTDMPPTTE 480  
QY 481 VTIDIVEMRENE 492  
D 481 VTIDIVEMRENE 492  
RESULT 13  
ADB73513  
ID ADB73513 standard; protein; 492 AA.  
AC ADB73513;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human PRO polypeptide #2.  
XX  
KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
cell death; neuropathy; neuropathy related disease;  
Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;  
XX chromosome mapping; gene mapping; genetic disorder; septic shock;  
antibacterial; immunosuppressive; neuroprotective.  
XX  
OS Homo sapiens.  
XX  
PN US2003045482-A1.  
XX  
PD 06-MAR-2003.  
XX  
PF 16-OCT-2001; 2001US-00978608.  
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XX 17-OCT-1997; 97US-0062250P.  
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PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
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PR 22-APR-1998; 98US-0082700P.  
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PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
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26-JUN-1998; 98US-00105413.  
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PR 02-NOV-1998; 98US-00184216.  
PR 06-NOV-1998; 98US-00187368.  
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PR 22-DEC-1998; 98US-00218517.  
PR 23-DEC-1998; 98US-0113296P.  
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PR 05-JAN-1999; 99WO-US000106.  
PR 05-MAR-1999; 99US-00254465.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99US-00265686.  
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PR 12-MAR-1999; 99US-00267213.  
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PR 14-MAY-1999; 99US-00311832.  
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PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 16-JUN-1999; 99US-0139557P.  
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PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380142.  
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PR 30-NOV-1999; 99WO-US028313.  
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PR 16-DEC-1999; 99WO-US030095.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 11-FEB-2000; 2000WO-US000376.  
PR 18-FEB-2000; 2000WO-US003565.  
PR 24-FEB-2000; 2000WO-US004341.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 21-MAR-2000; 2000WO-US006319.  
PR 30-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000US-00709238.  
PR 27-NOV-2000; 2000US-00723749.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US0005520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 22-MAR-2001; 2001US-00816920.  
PR 22-MAR-2001; 2001US-0089552.  
PR 10-MAY-2001; 2001US-00854208.  
PR

10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 30-JUL-2001; 2001US-00918585.  
XX (GETH ) GENENTECH INC.  
XX  
XX  
Query Match 100.0%; Score 2527; DB 7; Length 492;  
Best Local Similarity 100.0%; Pred. No. 1.4e-285;  
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XX AC ADB76229;  
XX DT 04-DEC-2003 (first entry)  
XX DE Human PRO polypeptide #2.  
XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW cell death; neuropathy; neuropathy related disease;  
KW Charcot-Marie-Tooth disorder; Reifsum's disease; Krabbe's disease;  
KW chromosome mapping; Gene mapping; genetic disorder; septic shock;  
KW antibacterial; immunosuppressive; neuroprotective.  
XX OS Homo sapiens.





PR 20-DEC-2000; 2000WC-US034956.  
PR 28-FEB-2001; 2001WC-US006520.  
PR 22-MAR-2001; 2001WC-US009552.  
PR 25-MAY-2001; 2001WC-US017092.  
PR 01-JUN-2001; 2001WC-US017800.  
PR 20-JUN-2001; 2001WC-US019692.  
PR 29-JUN-2001; 2001WC-US021066.  
PR 09-JUL-2001; 2001WC-US021735.  
PR 30-JUL-2001; 2001US-00918585.  
XX (GETH ) GENENTECH INC.  
PA  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
PI Stewart TA, Tumas D, Williams PM, Wood WI;  
XX  
DR WPI; 2003-755118/71.  
DR N-PSDB; ADB76228.  
XX  
XX New PRO polypeptides useful for treating peripheral neuropathy,  
PT neuropathies associated with systemic disease such as post-polio syndrome  
PT or AIDS-associated syndrome.  
XX  
XX Claim 12; Fig 4; 425pp; English.  
XX  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for  
CC identifying agonists or antagonists. The bioactive molecule may be a  
CC toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides  
CC are useful for treating neuropathy and neuropathy related diseases such  
CC as Charcot-Marie-Tooth disorder, Refsum's disease, and Krabbe's disease.  
CC The polynucleotide sequences encoding PRO polypeptides are useful as  
CC hybridisation probes, in chromosome and gene mapping, in the generation

Query Match 100.0%; Score 2527; DB 7; Length 492;  
Best Local Similarity 100.0%; Pred. No. 1.4e-285;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 PAFDKNPNKLVSTSTNTVAHKKFTFCVMSLSLTLCFVMEWTNVSEKILIDIIIGVD 360  
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DB 361 FAFALCVPLRIFSPFPVPTVRAHITGWLMTLTKTFFVLAPSSVLRRIIVLIASLVLPY 420  
QY 421 LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKQKKKMNESATGEDSAMTDMPTTE 480

Db 421 LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKQKKKMNESATGEDSAMTDMPTTE 480  
QY 481 VTDIVEMREENE 492  
Db 481 VTDIVEMREENE 492  
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XX AC ADC43655;  
XX AC ADC43655;  
DT 18-DEC-2003 (first entry)  
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XX Human; secreted protein; transmembrane protein; PRO; cytostatic;  
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;  
KW auditory; tumour growth; retinal disorder; sports-related joint problem;  
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;  
KW wound healing; hearing loss.  
XX Homo sapiens.  
XX US2003054986-A1.  
XX 20-MAR-2003.  
XX 16-OCT-2001; 2001US-00981915.  
PR 17-OCT-1997; 97US-0062250P.  
PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
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PR 11-MAR-1998; 98US-0077641P.  
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PR	29-APR-1998	98US-0083558P.	PR	30-NOV-1999	99US-0162506P.
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GenCore version 5.1.6  
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1104.347 Million cell updates/sec

Title: US-09-978-188A-7

Perfect score: 2527

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
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- 6: /cgn2\_6/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	812	32.1	162	4	US-09-489-847-160
3	586	23.2	114	4	US-09-489-847-321
4	118.5	4.7	518	4	US-09-134-001C-4744
5	109.5	4.3	610	3	US-08-970-725-2
6	108.5	4.3	361	3	US-09-196-520-6
7	104.5	4.1	610	1	US-08-212-188-2
8	104.5	4.1	610	5	PCT-US95-02708-2
9	104	4.1	536	4	US-09-107-532A-5507
10	103	4.1	631	4	US-09-107-532A-3902
11	103	4.1	1058	2	US-08-687-289A-5
12	103	4.1	1058	4	US-09-435-897-5
13	101.5	4.0	877	4	US-09-543-681A-6388
14	100.5	4.0	413	4	US-09-540-236-3672
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45	91.5	3.6	451	4	US-09-328-352-7659	Sequence 7659, Ap

ALIGNMENTS

RESULT 1

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; Sequence 320, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: P2031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
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; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-847-320

Query Match 42.1%; Score 1063; DB 4; Length 207;  
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Db 412 DTILNLVGNWAGGAAPSPULVLYSLYWKDUTRAGASG-----MWAGAVV 457  
QY 411 LIASLVLPYLGVRGATILGVGSLLAGFVGESTMVAIAACVYRKQKKMEN 461  
Db 458 VIVWISMIKPLATINAFPGMYEIIIPGFI-----VSVLITIVSKLTKKPPD 503

RESULT 5  
US-08-970-725-2  
; Sequence 2, Application US/08970725  
; Patent No. 6080542  
; GENERAL INFORMATION:  
; APPLICANT: Becker, Jeffrey M.  
; APPLICANT: Stacy, Gary  
; TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WEISER & ASSOCIATES  
; STREET: 230 South Fifteenth Street, Suite 500  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/970,725  
; FILING DATE: 14-NOV-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,188  
; FILING DATE: 16-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weiser, Gerard J.  
; REGISTRATION NUMBER: 19,763  
; REFERENCE/DOCKET NUMBER: 372.6601P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-875-8383  
; TELEFAX: 215-875-8394  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 610 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
US-08-970-725-2

Query Match 4.3%; Score 109.5; DB 3; Length 610;  
Best Local Similarity 18.9%; Pred. No. 0.0034;  
Matches 110; Conservative 93; Mismatches 172; Indels 207; Gaps 29;

QY 7 LTHYVPLRFVLPLGITHIADFGQALNR-----GT-----AAVKE--DAV 46  
Db 132 LSNFTFCVTPVGAALIA-----DQFLGRNTIVCSAVIIFIGLILITCTAIPSVIDAG 187  
QY 47 ENLASVGLAYSLMKFTGPMSPDKNVGLV-----FVNSKDRTKAVLCHVAGAI 96  
Db 188 KSMGGFVWSLIIIGLGTGK--SNVSPLMABQLPKIPPVYKTKGSKVIVDPWT--- 242  
QY 97 AAVFHTLAYSDLGYIINKLHVDESIGS-----KTRAFLYLAAPFMDAWT 147  
Db 243 -----TSRAYM-IFWTIN-----VGSUSVLAATTSLSTKGFVAYLLPL----- 281  
QY 148 HAGILLKHKYSFLVGCASISDVIAQVFWVAILLHSHLECREPLPIPLISLVNGALVRCCT 207  
Db 282 -----CVFVPLI-----ILAVSKTFTSTLLPPVPSLFV--LVKCSS 317  
QY 208 LCLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALILATORISRPYVNLVSRDLG 267

Db 318 LLL--KTNL-----ISKLNH-----LALLLLERYVKQWDDLFID-ELX 354  
QY 268 GSSAATEAVAILTATYVPVGHMPYGLTETRAVYPAFDKNNPSNKLVSNTVTAHI--- 324  
Db 355 RALRACKTFLF-----YPIYVVCYQGT-----NNLSIQAGQMOTGNVND 395  
QY 325 --KKTFVCMALSLTLC-----FVMTWTPNVSEKILIDI-IGVDRA----- 362  
Db 396 LFQAFDSIALIIFIFICDNIYPLRKYNIPKPIRITLGFMTATASMIYAAVLOAKIY 455  
QY 363 -----FAELCV-----VPLRIFSPFPVTVRAHLTGWLMTLKKTFVLPASV 405  
Db 456 QRGPCVANFTDTCVNDISVWIOIPAYVLIAPS---EIFASITG---LEPAFTKAPPSM 508  
QY 406 LRII-----VLIASLVLPYLGVRGATILGVGSLLAGFVGESTMVAIAACY 450  
Db 509 KSIITALLFTNAFGAIIISICISSTAVNPKLTWMTGTGAVTAPIAG-----IMFWUCF 561  
QY 451 VYRKQKKMENESATEGEDSAMTMDPPTTEEVTDIVEMRENE 492  
Db 562 HHYDAMEDEQNQLEFKRND-ALTKKDVEKVEHDSYMADESQ 602

RESULT 6  
US-09-196-520-6  
; Sequence 6, Application US/09196520  
; Patent No. 6204039  
; GENERAL INFORMATION:  
; APPLICANT: Falco, Carl S.  
; APPLICANT: Allen, Stephen M.  
; TITLE OF INVENTION: Plant Isocitrate Dehydrogenase Homologs  
; FILE REFERENCE: BB-1291  
; CURRENT APPLICATION NUMBER: US/09/196,520  
; CURRENT FILING DATE: 1998-11-19  
; EARLIER APPLICATION NUMBER: 60/067,388  
; EARLIER FILING DATE: December 2, 1997  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 361  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (68)  
US-09-196-520-6

Query Match 4.3%; Score 108.5; DB 3; Length 361;  
Best Local Similarity 21.4%; Pred. No. 0.0019;  
Matches 63; Conservative 49; Mismatches 86; Indels 97; Gaps 15;

QY 30 GEQALNRGIAAVKEDAVEMLASVGLAYSLMKFTGPMSPDKNVGLVFNKDRTKAVLC 89  
Db 105 GHRSLN--LTLRKE--LNLVYVRPCYSL-----PGYKTYRDNVNLITI---RENTG--- 150  
QY 90 MVVAGIAAVFHTLIAYSDLGYIINKLHVDESIGSKTRRAFLVLAAPFMDAMAWTHA 149  
Db 151 -----FYSGLEHQV---RGVYESLKITROASLRVAEYAFHYAKHGRE 192  
QY 150 GILLKHKYS-----FLVGCASISDVIAQVFWVAILLHS--HLECREPLIPII---S 196  
Db 193 RVSAIHKANIMQKTDLGFLKCCREVAEKYPEITYBEWIDNCMMVLMKPNALPDLVMPN 252  
QY 197 LYMGALVRCCTTLCGYV-----KNHIDIIPDRSGPELGGDATIRKM 237  
Db 253 LY-GDII--SDLCAGLVGGLGTSPCNIGEGGIALAEAVHGSAPDIAGKNLAN----- 302  
QY 238 LSPFWPLALILA-----TQRISRPVNL-----FVSRDLGGSSAATE 274  
Db 303 -----FTALLSGVTMLRHLNLHDKAEQIQKAILNTIAEGKYRTADLOGSSKTE 352

RESULT 7

```
US-08-212-188-2
; Sequence 2, Application US/08212188
; Patent No. 5689039
; GENERAL INFORMATION:
; APPLICANT: BECKER, JEFFREY M.
; APPLICANT: STACEY, GARY
; TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVE., N.W.
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,188
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 7493-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORGANISM: Arabidopsis thaliana
; IMMEDIATE SOURCE:
; CLONE: ATPR2ap
;
US-08-212-188-2
Query Match 4.1%; Score 104.5; DB 1; Length 610;
Best Local Similarity 18.5%; Pred. No. 0.013;
Matches 106; Conservative 96; Mismatches 169; Indels 211; Gaps 28;

Qy 7 LTHVPLRLFLVPLGINTNIAIDFGEQALNR-----GI-----AAVKE--DAV 46
Db 132 LSNFTFCWCVTPVGAALIA-----DQFLGRYNTIVCSAVIYFGILLTCTAIPSVIDAG 187

Qy 47 EMLASYGLAYSLMKFFGPMDFKNVGLV-----FVNSKRDRTKAVLCMVVAGAI 96
Db 188 KSMGGFVVSLIIIGLTGGIK--SNVSPLMAEQLPKIPPYVTKKNGSKVIVDPVVT---242

Qy 97 AAVFHTLLAYSDGLGYIINKLHHVDES VGS-----KTRAFVLYLAAPFMDAMWT 147
Db 243 -----TSRAV-IPYWTIN-----VGSLSVLATTSLESTKGFVAYLLPL-----281

Qy 148 HAGILLKHKYSLVGCASISDVIAQVVFVAILHSHLECREPLIIPILSLYMGALVRCVT 207
Db 282 -----CVFVIPLI-----ILAVSKTAFSTTLPPVPVSLFV--LVKCS 317

Qy 208 LCLGYNNKHDIIPDRSGPELGGDATIRKMSFWPLALILATQRIISRPIVNLVFSRDLG 267
Db 318 LLL--KTNL-----ISKLNH---LALLLLERYVKDQWDDLFID-ELK 354

Qy 268 GSSAATEAVAILTATYPVGHMPYGLWTEIR-----297
Db 355 RALRACKTFELF-----YPIYWCYQMTNNKISQAGQMTGNVSNDLFQAFDSIALIIFIP 410

Qy 298 ----AVPAPDKNNPSNK-----LVSTNTVTAAHIK-----KFTFVCWA 333
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Db 411 ICNIIYPLLRKNIPFKILRITLGFMPATASMIYAAVLQAKIYQRGPCYANFTDTCVS 470
Qy 334 LSLTL-----CFVFWTNPVSEKILIDIGVDFAFACELCWPLRIFSPFPVPTVRAHLT 388
Db 471 NDISVMIQIPAYVLI-----AFSEIFASITGLEFAFTK-----APPSMKSIIT 513
Qy 389 GWMTLTKKTFVLAPSSVLRIVLIASLVLPYLGVHGATLGVGSLLAGFVGESTMVAIAA 448
Db 514 ALFL-----FTNAFGAILSI--CISTAVNPKLTWMTYGTIAVTAFIAG-----IMFWV 559
Qy 449 CYVYRKQKKKXOMENESATEGEDSANTDMPPTVEEVTDIVEMRENE 492
Db 560 CFHHYDAMEDEQNLFEKRD-ALTKKDVEKEVHDSYMADESQ 602

RESULT 8
PCT-US95-02708-2
; Sequence 2, Application PC/TUS9502708
; GENERAL INFORMATION:
; APPLICANT: BECKER, JEFFREY M.
; APPLICANT: STACEY, GARY
; TITLE OF INVENTION: PLANT PEPTIDE TRANSPORT GENE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVE., N.W.
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02708
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 7493-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; IMMEDIATE SOURCE:
; CLONE: ATPR2ap
;
PCT-US95-02708-2
Query Match 4.1%; Score 104.5; DB 5; Length 610;
Best Local Similarity 18.5%; Pred. No. 0.013;
Matches 108; Conservative 96; Mismatches 169; Indels 211; Gaps 28;

Qy 7 LTHVPLRLFLVPLGINTNIAIDFGEQALNR-----GI-----AAVKE--DAV 46
Db 132 LSNFTFCWCVTPVGAALIA-----DQFLGRYNTIVCSAVIYFGILLTCTAIPSVIDAG 187

Qy 47 EMLASYGLAYSLMKFFGPMDFKNVGLV-----FVNSKRDRTKAVLCMVVAGAI 96
Db 188 KSMGGFVVSLIIIGLTGGIK--SNVSPLMAEQLPKIPPYVTKKNGSKVIVDPVVT---242

Qy 97 AAVFHTLLAYSDGLGYIINKLHHVDES VGS-----KTRAFVLYLAAPFMDAMWT 147
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Db 243 -----TSRAYM-IFYWTIN-----VGSLSVLATTSLESTKGFYVALLPL-----281
Qy 148 HAGILLKHYSFLVGCASISDVIAQVFFVAILLHSHLECREPLILPILSLYMGALVRCCT 207
Db 282 -----CVFVIPLI-----ILAVSKTFTSTLLPPVPSLFV--LVKCSS 317
Qy 208 LCLGYKNIHDIIPDRSGPELGSDATIRKMLSPWPLALILATORISRPVNLVFSRDLG 267
Db 318 LLL--KTNL-----ISKLNH---LALLLLERYKQDQDLDLFD-ELK 354
Qy 268 GSSAATEAVAILPATYPVGHMPYGMITEIR-----297
Db 355 RALRACKTFLF-----YPIYWCYQMTNNKISQAGQWQGNVNDLFOAFDSIALIIFTP 410
Qy 298 -----AYPAPDKNPNK-----LVSTSTVTAHKK-----KFTFVCWA 333
Db 411 ICNIIYPLLRKNIIPKPIRLITLGFMTATAMIAVLAQKIYORGPCYANFTDTCVS 470
Qy 334 LSLTL-----CFVMFWTPNVSEKILIDIGVDFAFACELCVPLRIFSPFPVTVRAHLT 388
Db 471 NDISVNIQIPAYVLI---AFSEIFASITGLEFAFK-----APPSMKSIIIT 513
Qy 389 GWMLTKKTFLVAPSSVLRIRIIVLILASLVLPYLGVHGATLGVCSLLAGFVGESTWVAIAA 448
Db 514 ALFL-----FTNAFGAILSI--CISSTAVNPKLWMTYTGIAVTAFAIAG-----IMFWV 559
Qy 449 CVYVRKQKKWENESAPTEGSDSAMTPPTEEVTDIVEMEENE 492
Db 560 CFHYDAMEDEQCLEFRND-ALTKDVEKEVHDSYSMADESQ 602

RESULT 9
US-09-107-532A-5507
; Sequence 5507, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5507:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...536
; SEQUENCE DESCRIPTION: SEQ ID NO: 5507:
US-09-107-532A-5507

Query Match 4.1%; Score 104; DB 4; Length 536;
Best Local Similarity 20.3%; Pred. No. 0.032;
Matches 82; Conservative 71; Mismatches 138; Indels 112; Gaps 19;

Qy 45 AVEMLASGLAYSLMKFTGP-MSDFKNVGLVFNVKRDRKAYL---CMVVGALIAAVF 100
Db 91 ALQWVGGLGLLFAFWIYASPLAHASGGBELIPTMRSLSIAVLVPPCMSVI-----143
Qy 101 HTLIAYSDLYIINK-----LHHVDESVGSKTRAFLYLAAPFMDAMWTHAGILLK 154
Db 144 -----RGYFQGNQEMMYALSQIVEQV---ARIFMLLATFIIMKVMGDFTVATQ 192
Qy 155 HKYSPLVGCASISDVIAQVFFVAILLHSHLECREPLILPILSLYMGALVRCCTTLCGLYK 214
Db 193 STFAPIG-----MLASILVLLYFLKGH-----QAYTSAFIH-----YSE 227
Qy 215 NIHDIPDRSGPELGSDATIRKMLSPWPLALILATORISRPVNLVFSRDLGSSAATE 274
Db 228 NKINI---ATKELLLD-TVKEAIPF-----IIVGSGVTIFKLVDFQFTFMKI--MSASTE 275
Qy 275 AVAILTATYPVGHMPYGMITEIRAVYPADFKNPNKLVSTSTVTAHKKFTFVCNML 334
Db 276 Y-----SNAQLDLFSIFSANPKLTWVIAL 302
Qy 335 SLTLCFVNFVTPNVSEKI-LIDIIGVDFAFACELCVPLRIFSPFPVTVRAHLTGWMLT 393
Db 303 ATSIAT--GLPLITEAVTLKDRVGL---AKLTSGNLQLEFSFFMFPATFGVMLLAYPL- 355
Qy 394 LKKTFLVAPSSVLRIRIIVLILASLVLPYLGVHGATLGVCSLLAG 436
Db 356 --NTLFYTPDSLGSNVLIQASVGL-FLGLY---MLVSNMLQG 392

RESULT 10
US-09-107-532A-3902
; Sequence 3902, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5507:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```



NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 3902:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 631 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...631  
SEQUENCE DESCRIPTION: SEQ ID NO: 3902:  
US-09-107-532A-3902

Query Match 4.1%; Score 103; DB 4; Length 631;  
Best Local Similarity 20.1%; Pred. No. 0.02;  
Matches 97; Conservative 60; Mismatches 167; Indels 158; Gaps 20;

QY 21 GITNIAIDGEGQALNRGIAVKEDAVEMLASVGL-----AYSLMKF 61  
DB 124 GILNSFIDW-----IAAVFAPTLGLVAGSLGKVLACTSNLLTTSSTGYIILNA 175  
QY 62 FTGPMSEDFKXNGLVFNKSRDRTKAVLCVWVAGATAAFAVHTLI-AYSGLGYIINKLHV 120  
DB 176 ADAPEFYFLPIFLAYTAAKFNTDFIANVIAAL--VYPTIVSAYSD----- 221  
QY 121 DESVSGKTRRAFLYLAAPFPDMAMATHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
DB 222 ----SITLR-FLGMPV-----ILARY-----TSTVIPAILAVVWYLS 252  
QY 181 HSHLECREPI-----LIPILSLYMGALV-RCTTLCGLGYKNIHDIIPDR 223  
DB 253 YIEPKIRKLSHSIRNLLTPFCIIWVFEIILLVGPDIADYASQLIAAGLYAVNFSPVL 312  
QY 224 SGPELGSDATIRKMLFWMPLALILATORISREPIVNLFVSRDLGGSSAATEAVAILTATY 283  
DB 313 SGAVIGGFQWLVFIPLHGLVPM-TNNLS-----FYGRDTLGPACMTAVAA----- 359  
QY 284 PVCHMPYGMWLTETRAVYPAFDK-NPNSKLVSTSTVTA-----AHKKFT 328  
DB 360 -----QAGAVLGWFLTKNKKVKSLSLAFITAFGITEPAVVGVTLYKRPFY 408  
QY 329 FVCMALSLTLCFYMFVTPNVSEKILIDIIGVDFAPAEALCVWPLRIFSPFPVPV-----T 382  
DB 409 IAC-----ICGAIFG-----GVAGA--AGAGALAVATRSITLSPFIVIGEGFVWL 450  
QY 383 VRAHLTGWMLTKKTFVLA-----PSSVLRILVILASLVLPYLGHGATLGVGSLLA 435  
DB 451 VASYFLAMISSCMLTFLFGYKDIEBESKDIVLSTPAAGEIIDLSEVNDPTFASGSLGE 510  
QY 436 GF 437  
DB 511 GF 512

RESULT 11  
US-08-687-289A-5  
Sequence 5, Application US/08687289A  
Patent No. 5981195  
GENERAL INFORMATION:  
APPLICANT: Fuller, Forrest H.  
APPLICANT: Krapcho, Karen J.  
APPLICANT: Hammerland, Lance G.  
TITLE OF INVENTION: CHEMERIC RECEPTORS AND METHODS FOR  
IDENTIFYING COMPOUNDS ACTIVE AT  
TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND

TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE  
TREATMENT OF NEUROLOGICAL DISORDERS  
TITLE OF INVENTION: AND DISEASES  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,289A  
FILING DATE: July 25, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/001,526  
FILING DATE: July 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 220/004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1058 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-687-289A-5

Query Match 4.1%; Score 103; DB 2; Length 1058;  
Best Local Similarity 20.3%; Pred. No. 0.045;  
Matches 75; Conservative 57; Mismatches 155; Indels 82; Gaps 21;

QY 110 GYIINKLHVDSVSGSKTRRAFLYLAAPFPDMAMATHAGILLKHYSFLVGCASISDV 169  
DB 477 GRDIMMLQYTEAN-----RYDYVHVGTW-HGVNLNIDDKYKIQM---NKSQM 519  
QY 170 IAQVVFVAILLHSHLECREPLIPIISLYMGALVRCITLCLGYKNIHDIIPDRSGPELG 229  
DB 520 VRSV-----CSEPLKQIKVIRKGEVSCWICTACKEN--EFVQD----- 558  
QY 230 GDATIRKMLFWMPLALILATORISREPIVNLFVSRDLGGSSAATEAV-AILTATYPVGHM 288  
DB 559 -EFTCRACDLGWPNAEALTGCEPI--PVRYLEWS-DIEGIALTLFAVLGFLFAVLG-- 612  
QY 289 PYGWLTEIRAVYPAFDKXNPSKLVSTSTVTAAHKKFTFVCMALSLTLCFY---MFWT 345  
DB 613 -----VFIRK-RNTP---IVKATNR-ELSYLLLPDLLC-CFSSSLFFIGEPQDWT 656  
QY 346 PNVSEKILIDIIGVDFAPAEALCVV--PLRIFSPFPVPVTVRAHLTGWMLTKKTFVLAPS 403  
DB 657 CRLRQ-----PAGGISFVLCISCLIVKTNRVLLVFEAKIPTSFHRKMWGLNLQFLVLC 711  
QY 404 SVLRILVILASLVLPYLGVHG-----ATLGVGSLLA-GFVGSTMTVAIAACYVR 453  
DB 712 TFMQIVICVILYTAAPPSSYRNQEBEIIFITCHEGSLMALGFLIGVYTCLLAAICFFFA 771  
QY 454 -KQKKQJEN 461  
DB 772 FKSRKLLEN 780

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RESULT 12
US-09-435-897-5
; Sequence 5, Application US/09435897A
; Patent No. 6534289
; GENERAL INFORMATION:
; APPLICANT: FULLER, FORREST H.
; APPLICANT: HAMMERLAND, LANCE G.
; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT METABOTROPIC GLUTAMATE
; TITLE OF INVENTION: RECEPTORS AND THE USE OF SUCH COMPOUNDS IN THE TREATMENT
; TITLE OF INVENTION: OF NEUROLOGICAL DISORDERS AND DISEASES
; FILE REFERENCE: 238/301
; CURRENT APPLICATION NUMBER: US/09/435,897A
; CURRENT FILING DATE: 1999-11-09
; EARLIER APPLICATION NUMBER: 08/687,289
; EARLIER FILING DATE: 1996-07-25
; EARLIER APPLICATION NUMBER: 60/001,526
; EARLIER FILING DATE: 1995-07-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1058
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized rat mGluR and human calcium receptor
US-09-435-897-5

Query Match 4.1%; Score 103; DB 4; Length 1058;
Best Local Similarity 20.3%; Pred. No. 0.045;
Matches 75; Conservative 57; Mismatches 155; Indels 82; Gaps 21;

QY 110 GYIINKLHVDESQVSKTRAPLYLAAPFMDAMATHAIIKHKYSFLVGCASISDV 169
DB 477 GRDIMMLQYTEAN-----RYDYVHVGTW-HEGVINIDYKIQM--NKSQM 519
QY 170 IAQVVFVAILHSHLECREPLIPILSLYMGALVRCITLCLGYKYNTHDIIPDRSGPELG 229
DB 520 VRSV-----CSEPLKQKQIVIRKGEVSCCWNICTACKEN--EFVQD----- 558
QY 230 GDATIRKMLSPWPIALILATORISRPVNLVFSRDLGGSSAATEAV-AITLTATYPVGHM 288
DB 559 -EFTCRACDLGWNAELTGCEPI--PVRYLEWS-DIEGALTUFAVLGIFLFAVLG-- 612
QY 289 PYGWLTEIRAVYPADKNNPSNKLVSSTNTVTAHAIKKFTVCMALSLTLCFV---MFWT 345
DB 613 -----VFIRK-RNTP--IVKATNR-ELSYLLLSLLC-CFSSSLFFIGEPQDWT 656
QY 346 PNVSEKILIDIGVDFAFAELCVV--PLRTFSFPFVPTVRAHLTGMLTKKTFVLAPS 403
DB 657 CRLRQ-----PAFGISFVLCISCIILVKTNRVLLVFEAKIPTSFHRKMWGLNLQFLVFL-C 711
QY 404 SVLRRIIVLIASLVLPVLGVHG-----ATLGVGSLLA-GFVGESTMVAIAACVYR 453
DB 712 TFMQIVICVILYTA PSSYRNQLEDEIIPITCHEGSLMALGPLIGYTCLLAICFFPA 771
QY 454 -KQKKMMEN 461
DB 772 FKSRKLPEN 780

RESULT 13
US-09-543-681A-6388
; Sequence 6388, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
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; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6388
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6388
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Query Match 4.0%; Score 101.5; DB 4; Length 677;
Best Local Similarity 20.4%; Pred. No. 0.032;
Matches 100; Conservative 60; Mismatches 143; Indels 187; Gaps 23;

QY 131 AFLYLAAPFMDAMAW-----THAGIL--LKHKYSFLVGCA----- 164
DB 140 AFYFILLFEMMSLASWFLVIADQDDSHAGLLVFFTAHAGSVLIMIAFFLWRESGSLD 199
QY 165 -----SISDVIAQVVFV-----AILHSHLECREPLIPILSLYMGALVRCIT 206
DB 200 FDSFRQLSLSPAMASVVELLGFPGFAGAKGMLPLHSLW----PKAHPAAPSHASALMSGV 255
QY 207 TILCLGYKYNTHDIIPDRSGPELGSDATIRKMLSPWPIALIL-----LATQR 252
DB 256 MVKIGIFGII-----KVGIDLLGAS-----QMWGIVVLAFGAVSVLVGWYALAEHD 303
QY 253 ISR-----PIVNLFVSRDLGGSSAATE-----AVAILTATYPV-----GRMPYGM 292
DB 304 LKRLLAHWHTVENIGIILMGVGVGMVGMATDPHVAALGLLGLYHLLNHAVFKGLFLGA 363
QY 293 LTEIRAVYPA-FDKNNPSNKLVSSTNTVTAHAIKKFTVCMALS----- 335
DB 364 GAIIINQIHRDMRDXMGGLAKLM--PYTATA-----FLIGMAISALPLPLNGFVSEWYTYQ 416
QY 336 --LTLCFVMFMPNVSEKILIDIGVDFAFAELCVVPLRIEFSF-----FPV 379
DB 417 SLFTSYSDGNFVRLSGPIAIIMLAITGALAAMCFVYGVVFCGPRSEQAKAKEVPL 476
QY 380 PTVTRAHLTGWL-----NTLKKTFVLAPS----- 404
DB 477 PMTIANGLLALFCVVLGVGAFAVPIIANIAMSSETSALTVTQAILVPSOAMFSP 536
QY 405 VLRIITVLIASLVLP---YLVGHG---ATLGVGSLLA-GFVGESTMVAIAACY----- 450
DB 537 ALTFILLTA-LPLIFLVLGLKGGQPAFRKGNPWACGYWEXKDMAYVAGGFTQALRSM 595
QY 451 ---VTRKQKK 457
DB 596 FAPLYMRKQ 605
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RESULT 14
US-09-540-236-3672
; Sequence 3672, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: GARY L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARI
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3672
; LENGTH: 413
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3672

Query Match 4.0%; Score 100.5; DB 4; Length 413;
Best Local Similarity 23.5%; Pred. No. 0.019;
Matches 80; Conservative 49; Mismatches 125; Indels 87; Gaps 20;
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QY 171 AQVVFVAIL-----LHSHUECREPLILPILSLYMGALVRCCTTLCGYGYNHDIIPDR-- 223  
DB 78 ATVLAIALISPPMGMLSDAVGRKPIVS--SULMLAL---PTALICMASSIHVEIFWRF 132  
QY 224 SGPELGGDATIKMLSFWMPLALIATORIS--PIVNLVFSRD--LGGSSAATEAVAILT 280  
DB 133 QGVSVPGITVV-----LAYISEEYSSRLTTMSLYVSGTVLGGFS----- 173  
QY 281 ATYFVGHMPY--GW-----LTEIRAVYPAFDKNPNKLVSTSTNTVTA-----AHI 324  
DB 174 GRFFAGHLEHFGWRYGYIWAICTLIGAIM--AYKSLPRSQNFTTPENFRFAFATLFSHT 232  
QY 325 KK-----FTFCMALSTLTCFVM-----FWTP--NVSEKILIDIIIGVDFAPAE 366  
DB 233 KNLHVICSFLGACVFLSVGGCTFINLHLSBSPYLLTPADLANIFAYLIG-----M 285  
QY 367 CVVPL--RIFSPFPVPT-----VRAHLTGWMLT--KTFVFLAPSSVLRIRIIVLIASLV 418  
DB 286 VITPLSTRVIREGMTSTILLAILVSTIGLMTLTFMPLGIVIMGLTMSGGVFIQSATI 345  
QY 419 PYLGVH--GATLGVGSLLAGFVGESTVVAIAACVYRKOK 456  
DB 346 SYLTVSHVSEGRSLASGLYMGYGGGFIGAWACALAYAGOK 386

## RESULT 15

US-09-252-991A-21730  
; Sequence 21730, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21730  
; LENGTH: 644  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21730

Query Match 4.0%; Score 100; DB 4; Length 644;  
Best Local Similarity 18.9%; Pred. No. 0.044;  
Matches 83; Conservative 77; Mismatches 175; Indels 104; Gaps 19;

QY 11 WPLIRFLVPLGITNIA-IDFGEOALNRGIAAVKEDAVEMLASYG-----LAYSIMKEFTGP 65  
DB 208 WPIFLFLAERLRNLGKYTFADVASYR-----LKQKQIRLSACGSLVWVAFYLIAMVGA 263  
QY 66 MSDFK-----NYGLVFVNSKDRDKAVLCMVVAGAIAA-----VFHTLIAYSDLGYYII 114  
DB 264 GKLELLFGLNYHVAVLVG-----ILWLYLVFGGMLATTWYQIIKAVLLLSGASFMAI 318  
QY 115 NKLHVDESQSKTRRAFLYLAAPPFMDAMANTHAGILLKHK-----YSFLVGCASIS 167  
DB 319 MVLKXVNFVDSTLPSEA---IKVHPKGEAI--MSPGGLVDRDIPSAFSLGFALMFGTAGLP 373  
QY 168 DVIAQVVFVAILLHSHUECREPLILPILSLYMGALVRCCTTLCGYGYNHDIIPDR-- 220  
DB 374 HILNRFVTS-----DAKEARKSVFY-----ATGFIQYVILTFIIGFAILL 416  
QY 221 -----PDRSGPELGGDATIRKVLSEFWPLALILATQIRSRPIVNLVSRDLGGSSAAT 273  
DB 417 VSTNPFDFKATGALIGN-----NMAAVHLADAVGGSLFLGFIASAVAFATILAV 465  
QY 274 EAVAILTATYPVGHMPYGLVTEIRAVYPAFDKNPNKLVSTSTNTVTAHIKKFTFCMA 333

DB 466 VAGLTLAGASAVSHDIYA-----SVFKG--GKANEXDEL-----RVSKMTTVALG 508  
QY 334 LSLTLCFVWFWPTNPNVSEKILIDIIIGVDFAPAEICVVPDLRIFSPFPVPTVR--AHLTGW-- 390  
DB 509 VVAIVLGIILPEKONIA-----FMVGLAFSAASCNFPVILLSNWYMKKLTTRGAMIGGWMG 563  
QY 391 LMTLKKTFFVLAPSSVLRIRI 409  
DB 564 LITAVGLMWLGPTIWWQIL 582

Search completed: April 22, 2004, 13:59:03  
Job time : 25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:57:59 ; Search time 48 Seconds  
(without alignments)  
2833.871 Million cell updates/sec

Title: US-09-978-188A-7

Perfect score: 2527

Sequence: 1 MVKFPALHYWPLRFLVPL.....TMDPTTEVTDIVEMRENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

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- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2527	100.0	492	9	US-09-978-192A-7
4	2527	100.0	492	9	US-09-978-832A-7
5	2527	100.0	492	10	US-09-978-189-7
6	2527	100.0	492	10	US-09-978-608A-7
7	2527	100.0	492	10	US-09-978-585A-7
8	2527	100.0	492	10	US-09-978-191A-7
9	2527	100.0	492	10	US-09-978-403A-7
10	2527	100.0	492	10	US-09-978-564A-7
11	2527	100.0	492	10	US-09-999-833A-7
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13	2527	100.0	492	10	US-09-978-824-7
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18	2527	100.0	492	10	US-09-978-757A-7
19	2527	100.0	492	10	US-09-978-187B-7
20	2527	100.0	492	10	US-09-978-643A-7
21	2527	100.0	492	10	US-09-978-375A-7
22	2527	100.0	492	10	US-09-978-298A-7
23	2527	100.0	492	10	US-09-978-188A-7
24	2527	100.0	492	10	US-09-978-681A-7
25	2527	100.0	492	10	US-09-978-194A-7
26	2527	100.0	492	10	US-09-999-829A-7
27	2527	100.0	492	10	US-09-978-299A-7
28	2527	100.0	492	10	US-09-978-544A-7
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30	2527	100.0	492	10	US-09-978-802A-7
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33	2527	100.0	492	12	US-10-013-917A-7
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35	2527	100.0	492	12	US-10-162-521A-7
36	2527	100.0	492	12	US-10-211-858-16
37	2527	100.0	492	12	US-10-145-016A-7
38	2527	100.0	492	12	US-10-145-088A-7
39	2527	100.0	492	12	US-10-145-092A-7
40	2527	100.0	492	12	US-10-145-129A-7
41	2527	100.0	492	12	US-10-165-039A-7
42	2527	100.0	492	12	US-10-165-353A-7
43	2527	100.0	492	12	US-10-167-600-7
44	2527	100.0	492	12	US-10-170-481A-7
45	2527	100.0	492	12	US-10-172-039A-7

#### ALIGNMENTS

#### RESULT 1

US-09-978-295A-7  
; Sequence 7, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertsien, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: ROY, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585

[illegible]

; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2527; DB 9; Length 492;
Best Local Similarity 100.0%; Pred. No. 7e-252; Indels 0; Gaps 0;
Matches 492; Conservative 0; Mismatches 0;

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Db 1 MVKPPALTHYPLRFLRPLVPLGTNTIAIDFGQALNRGIAAVKEDAVEMLASYGGLAYSLMK 60
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Db 61 FFTGPMSPFNKGLVFNKSKDRKXAVLCMVVAGIAAIVFTLTAYSDLGYYIINKLHV 120
QY 121 DESVGSKTRRFLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
Db 121 DESVGSKTRRFLYLAAPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180
QY 181 HSHLECREBLLPIILSLYMGALVRCTTCLGYKYNHDIIPDRSGPELGGDATIRKMLSF 240
Db 181 HSHLECREBLLPIILSLYMGALVRCTTCLGYKYNHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WPLALILATQISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGNLWTEIRAVY 300
Db 241 WPLALILATQISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGNLWTEIRAVY 300
QY 301 PAFDKNNPSNKLVSNTVTAHIIKKTFTVCNALSILTLCFVNFMTFNVSEKILIDIIIGVD 360
Db 301 PAFDKNNPSNKLVSNTVTAHIIKKTFTVCNALSILTLCFVNFMTFNVSEKILIDIIIGVD 360
QY 361 FAFaelCVVPLRIFSPFPVTVRAHLTGWLMTLTKKTFVLAPSSVLRIVLIASLVLPY 420
Db 361 FAFaelCVVPLRIFSPFPVTVRAHLTGWLMTLTKKTFVLAPSSVLRIVLIASLVLPY 420
QY 421 LGVHGATLGVGSLLAGFVGESTWVAIAACYVYRKQKKKNESATGEDSDSAMTDMPTTEE 480
Db 421 LGVHGATLGVGSLLAGFVGESTWVAIAACYVYRKQKKKNESATGEDSDSAMTDMPTTEE 480
QY 481 VTDIVEMREENE 492
Db 481 VTDIVEMREENE 492

RESULT 2
US-09-978-697-7
; Sequence 7, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
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; PRIOR APPLICATION NUMBER: 60/078939
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; PRIOR FILING DATE: 1998-03-26
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; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
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; PRIOR FILING DATE: 1998-03-30
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 100.0%; Pred. No. 7e-252; Mismatches 0; Indels 0; Gaps 0;  
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Sequence 7, Application US/09978192A  
Patent No. US2002017553A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC9  
CURRENT APPLICATION NUMBER: US/09/978,192A  
CURRENT FILING DATE: 2001-10-15  
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; APPLICANT: Ferrara, Napoleon
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A

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QY 241	WWPLALILATORISRPVNLVFSRDLGGSSAATEAVAIL	TATVPVGHMPYGLTEIRAVY	300		
DB 241	WWPLALILATORISRPVNLVFSRDLGGSSAATEAVAIL	TATVPVGHMPYGLTEIRAVY	300		
QY 301	PAFDKNNPSNKLVSNTVTAAHKKFTFCVMAISLTL	LCFVWFMTNVSEKILIDIIGVD	360		
DB 301	PAFDKNNPSNKLVSNTVTAAHKKFTFCVMAISLTL	LCFVWFMTNVSEKILIDIIGVD	360		
QY 361	FAPALCVPLRIFSPFPVTVVRAHLTGWLMTLKTFTVL	APSLSVLRITVLIASLVLPY	420		
DB 361	FAPALCVPLRIFSPFPVTVVRAHLTGWLMTLKTFTVL	APSLSVLRITVLIASLVLPY	420		
QY 421	LGVHGATLGVSLLIAGFVGSGSTWVAIAACVYPRKQ	KKQKNENESATGEDSAMTDMPPTSE	480		
DB 421	LGVHGATLGVSLLIAGFVGSGSTWVAIAACVYPRKQ	KKQKNENESATGEDSAMTDMPPTSE	480		
QY 481	VTDIVEMRENE	492			
DB 481	VTDIVEMRENE	492			
RESULT 5					
US-09-978-189-7					
; Sequence 7, Application US/09978189					
; Publication No. US20030004102A1					
; GENERAL INFORMATION:					
; APPLICANT: Ashkenazi, Avi					
; APPLICANT: Baker Kevin P.					
; APPLICANT: Botstein, David					
; APPLICANT: Desnoyers, Luc					
; APPLICANT: Eaton, Dan					
; APPLICANT: Ferrara, Napoleon					

/	PRIOR FILING DATE:	1998-03-30
/	PRIOR APPLICATION NUMBER:	60/080105
/	PRIOR FILING DATE:	1998-03-31
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/	PRIOR APPLICATION NUMBER:	60/085573
/	PRIOR FILING DATE:	1998-05-15
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/	PRIOR APPLICATION NUMBER:	60/085697

Query Match      100.0%; Score 2527; DB 10; Length 492;  
Best Local Similarity    100.0%; Pred. No. 7e-252;  
Matches 492; Conservative     0; Mismatches     0; Indels         0; Gaps             0;

QY	1	VVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAAYKEDAVEMLASYGSLMSLKF	60
Dd	1		

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QY 361 FAFELCVPLRIFSPFPVPTVRAHLTGWLTGKTFVLAPSSVLRIRIIVLIASLVLPY 420
Db 361 FAFELCVPLRIFSPFPVPTVRAHLTGWLTGKTFVLAPSSVLRIRIIVLIASLVLPY 420
QY 421 LGVHGATLGVSLLAGVSGSTWVAIAACVYVRKQKKMENESATEGSDSMTDMPTEE 480
Db 421 LGVHGATLGVSLLAGVSGSTWVAIAACVYVRKQKKMENESATEGSDSMTDMPTEE 480
QY 481 VTDIVEMREENE 492
Db 481 VTDIVEMREENE 492

RESULT 6
US-09-978-608A-7
; Sequence 7, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 7
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-7

Query Match 100.0%; Score 2527; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 7e-252;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKFPALHYWPLRFLPLGTNTAIDFGQALNRGIAAARKEDAVENMLASVGLAYSIMK 60
Db 1 MYKFPALHYWPLRFLPLGTNTAIDFGQALNRGIAAARKEDAVENMLASVGLAYSIMK 60
QY 61 FFTGPMSPDKNGLVFNKSRDRTKAVLCMVVAGAAVAFHTLIAYSGLGYIINKLHV 120
Db 61 FFTGPMSPDKNGLVFNKSRDRTKAVLCMVVAGAAVAFHTLIAYSGLGYIINKLHV 120
QY 121 DESVGSKTRAFVLYLAAPFFMDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAIL 180
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Db 121 DESVGSKTRAFVLYLAAPFFMDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAIL 180
QY 181 HSHLECREPLIPILSLYMGALVRCCTTCLGYKXNIIHDIIPDRSGPELGGDATIRKMLSF 240
Db 181 HSHLECREPLIPILSLYMGALVRCCTTCLGYKXNIIHDIIPDRSGPELGGDATIRKMLSF 240
QY 241 WPLALIIATQRIISRPINLVFVSRDLGSSAATAVAAILTATYPVGHMPYGLWTEIRAVY 300
Db 241 WPLALIIATQRIISRPINLVFVSRDLGSSAATAVAAILTATYPVGHMPYGLWTEIRAVY 300
QY 301 PAFDKNPNKLVSTNTVTAAHIKKFTFVCWALSLLTLCFVWFMTPNVSEKILIDIIGVD 360
Db 301 PAFDKNPNKLVSTNTVTAAHIKKFTFVCWALSLLTLCFVWFMTPNVSEKILIDIIGVD 360
QY 361 FAFELCVPLRIFSPFPVPTVRAHLTGWLTGKTFVLAPSSVLRIRIIVLIASLVLPY 420
Db 361 FAFELCVPLRIFSPFPVPTVRAHLTGWLTGKTFVLAPSSVLRIRIIVLIASLVLPY 420
QY 421 LGVHGATLGVSLLAGVSGSTWVAIAACVYVRKQKKMENESATEGSDSMTDMPTEE 480
Db 421 LGVHGATLGVSLLAGVSGSTWVAIAACVYVRKQKKMENESATEGSDSMTDMPTEE 480
QY 481 VTDIVEMREENE 492
Db 481 VTDIVEMREENE 492

RESULT 7
US-09-978-585A-7
; Sequence 7, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 7
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-7

Query Match 100.0%; Score 2527; DB 10; Length 492;
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Best Local Similarity 100.0%; Pred. No. 7e-252;			
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	MVKPALTTHYPLRFVPLGITHIAIDFGQALNRGIAAVKEDAVEMLASYGSLMK	60
Qy	61	FFTGPMSDFKNVGLVFNVSKDRTKAVLCMVVAGIAAAPHHTLIAYSDGLGYIINKLHHV	120
Db	61	FFTGPMSDFKNVGLVFNVSKDRTKAVLCMVVAGIAAAPHHTLIAYSDGLGYIINKLHHV	120
Qy	121	DESVGSKTRRAFLYLAAPFNDMAWTHAGILLKHKYSFLNGCCASISDVIAQVVFVAILL	180
Db	121	DESVGSKTRRAFLYLAAPFNDMAWTHAGILLKHKYSFLNGCCASISDVIAQVVFVAILL	180
Qy	181	HSHECREPLIPIILSLYMGALVRCTTLCGLGYKNIHDIIPDRSGPELGGDATIRKMLSF	240
Db	181	HSHECREPLIPIILSLYMGALVRCTTLCGLGYKNIHDIIPDRSGPELGGDATIRKMLSF	240
Qy	241	WPLALIIATORISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVY	300
Db	241	WPLALIIATORISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVY	300
Qy	301	PAFDKNTSPNKLVSNTVTAHKKKTFVCMALSLTLCFVWFMTNPNVSEKILIDIIGVD	360
Db	301	PAFDKNTSPNKLVSNTVTAHKKKTFVCMALSLTLCFVWFMTNPNVSEKILIDIIGVD	360
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Db	361	PAFALCVVPLRIFSPFPVTVRAHLTGWLTKKTFVLAAPSSVLRIVLIASLWLPY	420
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Db	421	LGVHGATLGVGSLLAGFVCESTWVAIAACVYVRKOKKXENESATGEDEDSAMTDPPTEE	480
Qy	481	VTDIVEMREENE 492	
Db	481	VTDIVEMREENE 492	

RESULT 8  
US-09-978-191A-7  
; Sequence 7, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC4  
; CURRENT APPLICATION NUMBER: US/09/978,191A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
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DB 61 FETGPMSPDKVGLVFNNSKEDRTKAVLCMVVAGAAVAFHTLIAYSDLYGYYIINKLHV 120  
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DB 301 PAFDKNPNKLVSTNSNTVTAHKKFTVCWALSLTLCFVWFPTNPVSEKILIDIIIGVD 360  
QY 361 FAFaelCVVPLRIFSPFPVPTVRAHLTGWLMTLTKKTFVLPAPSSVLRIRIIVLASLVLPY 420  
DB 361 FAFaelCVVPLRIFSPFPVPTVRAHLTGWLMTLTKKTFVLPAPSSVLRIRIIVLASLVLPY 420  
QY 421 LGVHGATLGVGSLLAGFVCESTWVAIAACVYVRKOKKXENESATEGSDSAMDMPPTTEE 480  
DB 421 LGVHGATLGVGSLLAGFVCESTWVAIAACVYVRKOKKXENESATEGSDSAMDMPPTTEE 480  
QY 481 VTDIVEMRENE 492  
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; Sequence 7, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavik, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
CURRENT FILING DATE: 2002-03-19  
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PRIOR FILING DATE: 2001-07-30  
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2527; DB 10; Length 492;
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RESULT 10
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; Sequence 7, Application US/09978564A
; Publication No. US20030050241A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C25
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; CURRENT FILING DATE: 2001-10-16
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; PRIOR FILING DATE: 2001-07-30
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68	PRIOR FILING DATE: 1998-05-15
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Query Match 100.0%; Score 2527; DB 10; Length 492;  
Best Local Similarity 100.0%; Pred. No. 7e-252;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11  
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Sequence 7, Application US/09999833A  
Publication No. US20030054405A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Giang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
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APPLICANT: Williams, P. Mickey

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; PRIOR FILING DATE: 1998-04-29  
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; PRIOR APPLICATION NUMBER: 60/084441  
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; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
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; PRIOR FILING DATE: 1998-05-07

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; PRIOR APPLICATION NUMBER: 60/084627  
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; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
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; PRIOR FILING DATE: 1998-05-07  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 2527; DB 10; Length 492;  
Best Local Similarity 100.0%; Pred. No. 7e-252;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MVKPPALTYWPLIRFLVPLGINTNIAIDFGEQALNRGIAA VKEDAVEMLASYG LAYSLMK 60  
Db 1 MVKPPALTYWPLIRFLVPLGINTNIAIDFGEQALNRGIAA VKEDAVEMLASYG LAYSLMK 60  
  
Qy 61 FFTGMSDFKNVGLVFNVNSKDRTKAVLCMVVAGATAA VFTHTLIAYS DGLGYIINKLHHV 120  
Db 61 FFTGMSDFKNVGLVFNVNSKDRTKAVLCMVVAGATAA VFTHTLIAYS DGLGYIINKLHHV 120  
  
Qy 121 DESVGSKTRRAFLYLAAPFPFMDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180  
Db 121 DESVGSKTRRAFLYLAAPFPFMDAMANTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180  
  
Qy 181 HSHLECREPLILPILSLYMGALVRC TTLCLGYKNYKNIHDIIPDRSGPELGSDATIRKMLSF 240  
Db 181 HSHLECREPLILPILSLYMGALVRC TTLCLGYKNYKNIHDIIPDRSGPELGSDATIRKMLSF 240  
  
Qy 241 WPLALILATORISRPVNLFSVSDICGSSNAATEAVAILTATYVGHMPYGLWLTETIRAVY 300  
Db 241 WPLALILATORISRPVNLFSVSDICGSSNAATEAVAILTATYVGHMPYGLWLTETIRAVY 300  
  
Qy 301 PAFDKNPSNKLVSSTNTVTAAHIKKFTFVCMALSLTL CFVMPWTPNVSEKILIDIIGVD 360  
Db 301 PAFDKNPSNKLVSSTNTVTAAHIKKFTFVCMALSLTL CFVMPWTPNVSEKILIDIIGVD 360  
  
Qy 361 PAFDELGVPLRIFSPFPVPTVRAHLTGWLNTUKTFLVLA PSSVLRIIVLIASLVLPY 420  
Db 361 PAFDELGVPLRIFSPFPVPTVRAHLTGWLNTUKTFLVLA PSSVLRIIVLIASLVLPY 420  
  
Qy 421 LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKOKKMMENESATEGEDSANTOMPTEE 480  
Db 421 LGVHGATLGVGSLLAGFVGESTWVAIAACVYVRKOKKMMENESATEGEDSANTOMPTEE 480  
  
Qy 481 VTDIVEMEENE 492  
Db 481 VTDIVEMEENE 492

RESULT 12  
US-09-981-915A-7  
; Sequence 7; Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PlC12  
CURRENT APPLICATION NUMBER: US/09/981,915A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
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PRIOR APPLICATION NUMBER: 60/077641  
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PRIOR APPLICATION NUMBER: 60/077649  
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PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
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PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
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PRIOR APPLICATION NUMBER: 60/078910  
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PRIOR APPLICATION NUMBER: 60/078939  
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PRIOR APPLICATION NUMBER: 60/079294  
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PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
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PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
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PRIOR APPLICATION NUMBER: 60/079728  
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PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
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PRIOR APPLICATION NUMBER: 60/083554

Query Match 100.0%; Score 2527; DB 10; Length 492;  
Best Local Similarity 100.0%; Pred. No. 7e-252;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVKFPALTHWPLRFLVPLGINTNIAIDFGEQALNRGIAA VKEDAVEMLASGLAYSLMK 60  
DB 1 MVKFPALTHWPLRFLVPLGINTNIAIDFGEQALNRGIAA VKEDAVEMLASGLAYSLMK 60

QY 61 FTGPMSEDFKQGLVFNKGRDRTKAVLCWVAGAI AAVFHTLIAYSDILGYIINKLHHV 120  
DB 61 FTGPMSEDFKQGLVFNKGRDRTKAVLCWVAGAI AAVFHTLIAYSDILGYIINKLHHV 120

QY 121 DESVSGKTRPAFLYLAAPFPMADAMANTHAGILLKHKYSFLVGCASISDVIAQVFWVAILL 180  
DB 121 DESVSGKTRPAFLYLAAPFPMADAMANTHAGILLKHKYSFLVGCASISDVIAQVFWVAILL 180

QY 181 HSHLECREPLLIPILSYMGALVRCITLCLGYGKNIHDIIPDRSGPELGGDATIRKQMSF 240  
DB 181 HSHLECREPLLIPILSYMGALVRCITLCLGYGKNIHDIIPDRSGPELGGDATIRKQMSF 240

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DB 241 WNPALILATORISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGLMTEIRAVY 300  
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DB 301 PAFDKNPNKLVSTNTVTAHAIKKFTFVCWALSITLCFVWFMTPNVSEKILIDIIGVD 360  
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DB 361 FAFaelCVVPLRIFSFPPVTVRAHLTGWLMTLKKTFVLAPSSVLRIVLIASLVLPY 420  
QY 421 LGVHGATLGVSLLAGFYGESTMVAIAACVYVRKOKKKNESATEGEDSAMTDMPTTEE 480  
DB 421 LGVHGATLGVSLLAGFYGESTMVAIAACVYVRKOKKKNESATEGEDSAMTDMPTTEE 480  
QY 481 VTDIVEMRENE 492  
DB 481 VTDIVEMRENE 492

RESULT 13  
US-09-978-824-7  
; Sequence 7, Application US/0978824  
; Publication No. US20030055216A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630FIC14  
CURRENT APPLICATION NUMBER: US/09/978,824  
CURRENT FILING DATE: 2001-10-17  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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PRIOR APPLICATION NUMBER: 60/066364  
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PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649

PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22
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PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-22
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PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704	PRIOR FILING DATE: 1998-05-15

; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
Query Match 100.0%; Score 2527; DB 10; Length 492;  
Best Local Similarity 100.0%; Pred. No. 7e-252;  
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MYKFPALHYWPLRFLVPLGLTNTIAIDFGEQALNRGIAAVKEDAVEMASYGLAYSLMK 60  
DB 1 MYKFPALHYWPLRFLVPLGLTNTIAIDFGEQALNRGIAAVKEDAVEMASYGLAYSLMK 60  
QY 61 FTGPMSPDKNGLVFNKSRDRTKAVLCMWVAGIAA VEHFTLIAYSDLYGIYIINKLHHV 120  
DB 61 FTGPMSPDKNGLVFNKSRDRTKAVLCMWVAGIAA VEHFTLIAYSDLYGIYIINKLHHV 120  
QY 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
DB 121 DESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
QY 181 HSHLECREPELLIPLISLYNGALVRCCTTCLGYKKNIHDIIPDRSGPELGGDATIRKMLSF 240  
DB 181 HSHLECREPELLIPLISLYNGALVRCCTTCLGYKKNIHDIIPDRSGPELGGDATIRKMLSF 240  
QY 241 WYPLALILATORISRPVNLFSRDLGGSSAATEAVAILTATYPVGHMPYGMWLTIRAVY 300  
DB 241 WYPLALILATORISRPVNLFSRDLGGSSAATEAVAILTATYPVGHMPYGMWLTIRAVY 300  
QY 301 PAFDKNPNKLVSTNTTAAHIKFTFVCMALSLTLCFVNFMTNPNVSEKILLIDIIGVD 360  
DB 301 PAFDKNPNKLVSTNTTAAHIKFTFVCMALSLTLCFVNFMTNPNVSEKILLIDIIGVD 360  
QY 361 FAFAEUCVPLRIFSPFPVTVRAHLTGWLTKTFLVAPSSVLRIVLIVIASLVLPY 420  
DB 361 FAFAEUCVPLRIFSPFPVTVRAHLTGWLTKTFLVAPSSVLRIVLIVIASLVLPY 420  
QY 421 LGVHGATLGVSLLAGFVGESTWVAIAACYVYRKQKKKNENESATEGEDSAMTDMPTTEE 480  
DB 421 LGVHGATLGVSLLAGFVGESTWVAIAACYVYRKQKKKNENESATEGEDSAMTDMPTTEE 480  
QY 481 VTDIVEMRENE 492  
DB 481 VTDIVEMRENE 492

## RESULT 14

US-09-918-585A-7  
; Sequence 7, Application US/0918585A  
; Publication No. US2003006046A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Flvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuc, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: F2630F1C1  
; CURRENT APPLICATION NUMBER: US/09/918,585A  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
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; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
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Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 DESVGSKTRRAFLYLAAPFFMDAMANTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180
Db 121 DESVGSKTRRAFLYLAAPFFMDAMANTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180

Qy 181 HSHLECREPLLIPIILSLYMGALVRCCTTLCGLYYKNHIDIIPDRSGPELGGDATIRKMLSF 240
Db 181 HSHLECREPLLIPIILSLYMGALVRCCTTLCGLYYKNHIDIIPDRSGPELGGDATIRKMLSF 240

Qy 241 WMLPLALILATORISRPINLVNLFVSRDLGGSSAAATEAVAILTATYPVGHMPYGLTIRAVY 300
Db 241 WMLPLALILATORISRPINLVNLFVSRDLGGSSAAATEAVAILTATYPVGHMPYGLTIRAVY 300

Qy 301 PAFDKNPNKLVSTNTVTAHHKFTFVCMALSLTLCFVNFVTPNVSEKILIDIIGVD 360
Db 301 PAFDKNPNKLVSTNTVTAHHKFTFVCMALSLTLCFVNFVTPNVSEKILIDIIGVD 360

Qy 361 FAFAEELCVVPLRIEFPFPPVTVRAHLTGWMLTKKTFVLAAPSSVLRIRIIVLTASLVLPY 420
Db 361 FAFAEELCVVPLRIEFPFPPVTVRAHLTGWMLTKKTFVLAAPSSVLRIRIIVLTASLVLPY 420

Qy 421 LGVHGATLGVGSLLAGFVGESTWVAIAACYVYRKQKKMENESATEGEDSANTDMPPTTEE 480
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Qy 481 VTDIVEMRENE 492
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; Publication No. US20030069178A1
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GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
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Db 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYYVRKQKKMENESATEGEDSANTDMPTEE 480  
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Db 481 VTDIVEMEENE 492

Search completed: April 22, 2004, 14:03:55  
Job time : 50 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2004, 13:54:13 ; Search time 20 Seconds  
(without alignments)  
2366.312 Million cell updates/sec

Title: US-09-978-188A-7

Perfect score: 2527  
Sequence: 1 MVKFPALHYWFLIRFLVPL.....TMDPPTEVTDIVRENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1: \*\*  
2: PIR2: \*\*  
3: PIR3: \*\*  
4: PIR4: \*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	183.5	7.3	449	AE1952	hypothetical prote
2	180.5	7.1	433	AH2337	hypothetical prote
3	119.5	4.7	693	C81078	carbon starvation
4	117.5	4.6	693	B81865	carbon starvation
5	115.5	4.6	670	S78182	NADH2 dehydrogenas
6	115	4.6	444	A71121	PTS betagluco-side-
7	115	4.6	507	B83988	proline transporte
8	114.5	4.5	447	F69433	conserved hypothet
9	113.5	4.5	512	B89078	high affinity prol
10	113.5	4.5	586	S02154	NADH2 dehydrogenas
11	112.5	4.5	398	AD0828	probable transmemb
12	112.5	4.5	497	T48676	proline uptake pro
13	111	4.4	622	E69609	cytochrome-c oxida
14	110.5	4.4	400	AB0967	probable membrane
15	110.5	4.4	452	AB1437	PTS system, cellob
16	108.5	4.3	427	C82221	conserved hypothet
17	108.5	4.3	450	AC1079	PTS system, cellob
18	108.5	4.3	492	AC0768	probable transmemb
19	108	4.3	444	AI1481	PTS betagluco-side-
20	108	4.3	740	AB0600	probable membrane
21	107	4.2	416	JT0487	lactose permease -
22	107	4.2	422	A69853	hexuronate transpo
23	106	4.2	334	A64447	hypothetical prote
24	105.5	4.2	372	T48350	3-isopropylmalate
25	105	4.2	404	H64175	hypothetical prote
26	105	4.2	561	AG3119	ABC transporter, m
27	105	4.2	561	H98167	hypothetical prote
28	105	4.2	592	H97105	carbon starvation
29	105	4.2	1019	B71874	probable cation ef

30 104.5 4.1 415 2 C84829  
31 104.5 4.1 467 2 F83009  
32 104 4.1 417 2 D90678  
33 104 4.1 417 2 H85528  
34 103.5 4.1 398 1 E64112  
35 103.5 4.1 551 2 F83241  
36 103 4.1 417 1 GREG  
37 103 4.1 501 2 T44298  
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39 102.5 4.1 446 2 AD0509  
40 102.5 4.1 446 2 S22614  
41 102.5 4.1 641 2 S63645  
42 102 4.0 537 2 AI1640  
43 102 4.0 539 2 E97025  
44 102 4.0 1020 2 A64641  
45 101.5 4.0 446 2 B42661

ALIGNMENTS

RESULT 1

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hypothetical protein all1168 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AE1952  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yaeuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE1952  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-449 <KUR>  
A:Cross-references: CB:BA000019; PIDN:BB73125.1; PID:gl7130514; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all1168

Query Match	7.3%	Score	183.5	DB	2	Length	449
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Db	25	LITQFIPLSLSDVAMTLDPLQTSALSR	--	ETLAGVGVKGVAVFLESPIIM	79		
QY	69	PKNVGLVFNVNSKRDRTRAVLCMVVAGIAAVFHTLIAYSDLGYYIIINKLHHVDESUGSKT	128				
Db	80	ILHASTALGGQAKSRRLAQWQTIITAGLVLSQIFLLLTWEPLYNLLLDVFGVSSLIQORG	139				
QY	129	ERAFILYLAAPFPMDAMAWTHAGILLKHYSFLVGCASISDVIAQVFWFVAILLHSHLECRE	188				
Db	140	RTAFELMFLWPFVIAWRPFQGLLIRAKSTAVGASVARLTWVSVLVGVNLRDGM	199				
QY	189	FLILPILSYMGALVRCITCLGYKYNKHIDIIIPDRSGP	---	ELGGDATIRKM	---	L	238
Db	200	LAGITMGAIIIEAVLVTFCL	---	RLGAISILEQQGYSETKKLPQTJSGV	247		
QY	239	SFWW-PILALILATQIRSPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGLWTEI	-	296			
Db	248	SFYLPPLASTMLVWGARAIIISLIARSFDGSL	---	ALAVWPAT	---	WGLLSIA	296
QY	297	-----RAVTPAFDKNNPSNKLVSNTVTAAHKKFTFVCMALSLTLCFVFMFWPNVS	349				
Db	297	NGTRMIQQVVISAYEE	-----	TSRRTLAAFV	-----	IIVGLSFTLIPFLGFTDQG	342
QY	350	EKILIDIGVDFAPABLCVPLRIFSPFPVTVRAHLTGMLTKTKTFLVAPSSVLR	--	407			
Db	343	LFLLRQFLGNPFLSVLEASRPVIQILSCFPLLLALQNTFQGLLIHKGNWFLNATVVAAT	402				

xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V.  
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
A:Reference number: AB1000; MUID:20175755; PMID:10710307  
A:Accession: C81078  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-693 <TET>  
A:Cross-references: GB:AB002498; GB:AB002098; NID:g7226724; PIDN:AAF41849.1; PID:g722672;  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1493  
C:Superfamily: carbon starvation protein

Query Match 4.7%; Score 119.5; DB 2; Length 693;  
Best Local Similarity 22.2%; Pred. No. 0.077;  
Matches 111; Conservative 69; Mismatches 181; Indels 139; Gaps 26;  
QY 12 PLIRFLVPLGINTIAIDFGE-QALNRGTAAYKEDAVEMLASVGLAYSLMKFTGPMSPDK 70  
DB 270 PVMLLTTPRDVLTSTKIGTIAALGIVIV-NPALQMPAVTHFDGSGPVPFSGALPFF- 327  
QY 71 NVGLVFNKRDRTKAVLCMVVAGAAVFTHTLAYSGLGYIINKLHHVDESVEGSKTRR 130  
DB 328 ----LFI-----TIAGVSG-----FHALISSGTPKMLENETHVRMIGYGMLE 370  
QY 131 AFYLAAPFFMDAMAWTHAGI-LLKHYSFLVGCASISDVIAQV-----VFVAILLH 181  
DB 371 SFVAIMA---LAAASALDPGVVFAMNSPALITG--TDANTAAREVITTKLOFPVDAATLLH 425  
QY 182 SHLECREPLLIPILSLYMGALVRCCTLCGLGYKNIHDIIPDRSGPELGGDATTIRKMLGF 241  
DB 426 TAKEGEN---TILSRAGA---PTLAVGMHINSRLIP-----GEA-----MMAFW 466  
QY 242 WPLALIL-----ATQISRPVNLVFSRDJGG-----SSAATEAVAILTAT 282  
DB 467 YHFAALLFEALFILTAVDAGTRVAR-----FMQDLGSIYKPFPGNTDSTIPANLIATFFAV 521  
QY 283 YPVGMHPYGLWTE---IRAVYPAEDKKNPSKNKLVSTNTVTAHKKFTFVCMALSLTL 338  
DB 522 ALMGFLYTGVTDPGLGINSMLPLF-----GIANQMLA-----GVALLM 560  
QY 339 CFVWF-----WTPNVSEKILIDIIGVDFAPAFELCVPLRIFSPFFPVVTVRAHUTG 389  
DB 561 CAVVLIKMKRDRVWV-----VLVPVGVLEV---TCVAGLQKLFHSDPRISFLAHAGK 611  
QY 390 WMLTKKTFVLAPS-----SVLRIL-----VLIALSVLPVGLVGHGATLGVGSLIA 435  
DB 612 YSDALAKNEILAPAKDIGEMAOIIFNDKINAGLTILFLSVVVI---VAAYGLRT---ALKA 666  
QY 436 GFVGESTWVAIAACYVVRKQ 455  
DB 667 RKVGWPTAKEIPAVYRDGKQ 686

RESULT 4  
E81865  
carbon starvation protein A homolog NMA1698 [similarity] - *Neisseria meningitidis* (stra  
C:Species: *Neisseria meningitidis*  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: E81865  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More  
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A:Reference number: AB1775; MUID:2022556; PMID:10761919  
A:Accession: E81865  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-693 <PAR>  
A:Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CBM84926.1; PID:g73803.  
A:Experimental source: serogroup A, strain Z2491

QY 408 -IIVLASLVLPVGLVGHGATLGVSLLAGFVGESTWVAIA 447  
DB 403 FTLVICGSLIFTHSGATSAAYG---MLAGVSEIIVFLFA 440

RESULT 2  
AH2537  
hypothetical protein alr7587 [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120be  
C:Species: *Nostoc* sp. PCC 7120  
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AH2537  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AH2537  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-453 <KUR>  
A:Cross-references: GB:AP003602; PIDN:BA877230.1; PID:g17134672; GSPDB:GNC00181  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr7587  
A:Genome: plasmid

Query Match 7.1%; Score 180.5; DB 2; Length 453;  
Best Local Similarity 20.4%; Pred. No. 4.2e-07;  
Matches 94; Conservative 91; Mismatches 206; Indels 69; Gaps 15;  
QY 13 LIRFLVPLGINTIAIDFGEQALNRGTAAYKEDAVEMLASVGLAYSLMKFTGPMSPDKV 72  
DB 34 LLKQFIPLSLSDVAMTLDPLQTSLSLSPQ-ETLAGVGWVGVAFLSPSIIMILHA 92  
QY 73 GLVFNKRDRTKAVLCMVVAG-ALAAVFTHTLAYSGLGYIINKLHHVDESVEGSKTRR 131  
DB 93 STALGGQAKSRVLMQFTVIAAGLALSGIF-LFLWKPLYNMLLDDLPFGVSSIAARGTA 151  
QY 132 FLYLAAPFFMDAMAWTHAGIILKHYSFLVGCASISDVIAQVFWVAILLHSHLE- 185  
DB 152 FLLMFLPFWVIAWRFFQGLLIRAHKSIAVGWASVARUTWIVTLAVGVSURLDGAFLAG 211  
QY 186 -----CREPLLIPILSLYMGALVRCCTLCGLGYKNIHDIIPDRSGPELGGDATTIRKML 238  
DB 212 IFMGAILIEAVLWFLGRLGALSILNQ--QGVSET-----KKUPQTFGEVTF- 259  
QY 239 SPWWPLALILATQISRPVNLVFSRDJGSSAATEAVAILTATVPVGMHPYGLWTEI-- 296  
DB 259 -YVLPLASTMLLVGABAILLSLIARAFDGS-----IALAVMPAA---WGLLSIAN 306  
QY 297 -----RAVYPAEDKKNPSKNKLVSTNTVTAHKKFTFVCMALSLTLCFVWFVTPNVSE 350  
DB 307 GTRMIQQVVISAYEE-----TSRRTLAAV-----IIVGLSFTLIPFLGVTDQGL 352  
QY 351 KILIDIGVDPAFELCVPLRIFGFPVTVRAHGLTGLWMLT-KKTFVLAPS SVLRIL 409  
DB 353 FILRQFLGNPNLSVNASRPVQILCLPALLALQNTFQGLLTHKGNWFINLATIVRAIL 412  
QY 410 VII--ASLVLPVGLVGHGATLGVSLLAGFVGESTWVAIA 447  
DB 413 TLVVCGLTIFTRHSGANSAYG---MLAGVIGEIIVLFFFA 449

RESULT 3  
C81078  
carbon starvation protein A homolog NMB1493 [similarity] - *Neisseria meningitidis* (stra  
C:Species: *Neisseria meningitidis*  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: C81078  
R:Tetrelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

C:Genetics:  
A:Gene: NMA1698  
C:Superfamily: carbon starvation protein

Query Match 4.6%; Score 117.5; DB 2; Length 693;  
Best Local Similarity 22.3%; Pred. No. 0.11;  
Matches 100; Conservative 63; Mismatches 149; Indels 137; Gaps 24;

QY 62 FTGPMDFKNGLVFVNSKRDRTKAVLCWVAGAAAFVHTLIAYSDLGYYIINKLHVD 121  
DB 320 FSGALFPE-----LPI-----TIACAVSG-----FHALISSGTTPKMLENETHVRM 361

QY 122 ESVGSKTRRAFLYLAAPFMDAMAWTHAGI-LLKHYSFLVGCASISDVIAQV----- 173  
DB 362 IGYGMLMESFVAINA-----LAAASLDGVYFAMNSPAALIG--TDANTAEEVTTKLQF 416

QY 174 -VFVAILLHSHLECEPELLIPILSYMGALVRCCTTCLCGYYKNDHIIDPRSGPGLGDA 232  
DB 417 PVDANTLHTAKEVEN--TILSPAGG---PTLAVGMAHMSRLIP-----GEA 461

QY 233 TIRKMSFWPMLALIL-----ATQISRPVNLVFSRDJGG-----SSAAT 273  
DB 462 ---NMAFWYHFAALLFEALFILTAVDAGTRVAR-----FMQDLGSIYKPFNGNTDSTPA 512

QY 274 EAVAILTATYPVGHMPYGLWTE---IRAVPAEDKNPNKLVSTNTVTAAHKKFTF 329  
DB 513 NLIAFFFAVALMGYFLYTGVTDPGGINSMLPF-----GIANQMLA----- 554

QY 330 VCMALSLLTCFYMF-----WTPNVSEKILIDIIIGVDFAFALCVVPIRIFSPFPV 380  
DB 555 ---GVALLIMCAVLIKMKRDYVWV-----VLVPAGVLFV---TCVAGLQKLFHSDPR 602

QY 381 VTVRAHLTGWMLTKTFTVLAPS-----SVLRIT-----VLIASLVNLPVLGVHGA 426  
DB 603 ISFLAHTGYSDALAKNEVLAPAKDIGEMAQIIFNDKINAGLTILFLSVVVI--VAAYGL 660

QY 427 TLGVGSLLAGFVGESTVMAIACVYVRKQ 455  
DB 661 RT---ALKARKVGWTAKEIPAVYRDGKQ 686

RESULT 5  
S78182  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Reclinomonas americana (ATCC 50394)  
C:Species: mitochondrion Reclinomonas americana  
A:Variety: ATCC 50394  
C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 03-Jun-2002  
R:Bang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C.; Sank  
Nature 387, 493-497, 1997  
A:Title: An ancestral mitochondrial DNA resembling a eubacterial genome in miniature.  
A:Reference number: S78127; MUID:97311393; PMID:9168110  
A:Accession: S78182  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-670 <LAN>  
A:Cross-references: EMBL:AF007261; NID:92258325; PIDN:AAAD11915.1; PID:G2258381  
A:Experimental source: ATCC 50394  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997  
C:Genetics:  
A:Gene: nad5  
A:Genome: mitochondrion  
A:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 4.6%; Score 115.5; DB 2; Length 670;  
Best Local Similarity 19.1%; Pred. No. 0.16;  
Matches 94; Conservative 72; Mismatches 191; Indels 135; Gaps 19;

QY 5 PALTHYWPILRIFVPLIGTIN-----IAIDFGQALNRGIAAVKEDAV 46  
DB 111 PRMYSYLSLFTFFMLMLVITGDNFVQMFLGWEGVGLCSYLLINFWTRLOANKSAIKAMIM 170

QY 47 EMLASYGLAYSLMK-FTGPMDSDFKNV-----GLVFNVSKRDRTKAVLCWVAGA 95  
DB 171 NRIGDFGLSLGMAIFFTFKSVDFITVFALSPYMTDFNIIFENYEVHALTLCILLFVGA 230

QY 96 IAAV-----PHTLIAYSDLGYYIINKLHVDSEVGSKTRRAFLYLAAPFMD----- 142  
DB 231 VGKSSQLGHLTWLDPAMEGFTTPVSALIHAAWV---TAGVFLIARCSPIFEVAPTALLVV 287

QY 143 ---AMAWTHAGI-LLKHYSFLVGCASISDVIAQVVFVAILLHS-----HLECEPELLI 192  
DB 288 TIVGAMTAFAATTGLQNDIKRVIAYSTCSQLGVVVFACGISGYSVGMFHL----- 339

QY 193 PILSLYMGALVRCCTTCLCGYYKNDHIIDPRSGPGLGDATIRKMSFWPMLALILATQ 252  
DB 340 -MNAHAFKALLFLSAGCV-----IHALADEQDMRMGG---IVKLVFFYGMMLIGMSNL 390

QY 253 ISRPVNLVFSRDJGSSAATAEAVAILTATYPVGHMPYGLWTEIRAVYPAF----- 303  
DB 391 MGPFPLTGFSKDV-----ILELAFAKYITDGTFAHMLGTVAAPFTAFYSFRLIYLT 442

QY 304 ---DKNPNKLVSTNTVTAHIKXF--TFVCMALSLLTCFYMFVTPNVSEKILIDIIIG 358  
DB 443 FLGETNSP-----RTIINHARDAPFIMAFPLMLAVGSI FVGFI---VMKDMMIG-LG 490

QY 359 VDFAFALCVVPIRIFSPFPVTVRAHLTGWMLTKTFTVLAPSVLRIIVLIASLVVL 418  
DB 491 TDFWNSLTHPKN-----LTLIESEFIPTPKLLPVV----- 523

QY 419 PYLGVHGAATLV 430  
DB 524 --LSITGATLAI 533

RESULT 6  
AF1121  
PTS betaglucoside-specific enzyme IIC component homolog lmo0373 [imported] - Listeria mo  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AF1121  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AF1121  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-444 <GLA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC98452.1; PID:G16409751; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0373  
C:Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-depend

Query Match 4.6%; Score 115; DB 2; Length 444;  
Best Local Similarity 20.4%; Pred. No. 0.11;  
Matches 94; Conservative 69; Mismatches 151; Indels 146; Gaps 25;

QY 66 MSDFKNV-----GLVFNVSKRDRTKAVL-CWVAGAIAAVFHTLIAYSDLGYYIINKLH 119  
DB 10 VNGFINAQLGGQIHLSURDAPASIMPMLLAG-----FVTLI-----NYVILEPTGF 59

QY 120 VDESVGSKTRRAFLYLAAPFMDAMAWTHAGIILKHYSFLVGCASISDVIAQVVFVAIL 179  
DB 60 MGKIVNPDTLR-----TWQEIGI-----SIGNGTLS-VITLLVTVAIS 96

QY 180 LH-----SHLECEPELLIPILSLYMGALVRCCTTCLCGYYKNIH--DIIP-----DRSGPEL 228  
DB 97 YHLCINRGYNVIAPILVALSSFIWTPVTIAMTFLPEGASKSIEVPNVIPVSTGASGMVF 156

QY 229 G-----GDATIR-----KMLSFWMPLALILATORISRPVNL 261  
Db 157 GIIVGLTATDLFKLSKQKRMQINLTGNIPAVIKSNVLIPIIMITVIFSVMSFAVNI 216  
QY 262 VSRDLGG--SSAATEAVAILTATVPVGMPL--TEIRAVY-----PAFDK 305  
Db 217 FSDMNTLVITIIKPLSVYVTTSLP-----GFLITSIANLPFGLGHOAVISGILLDP 270  
QY 306 ---NNPSNKLVSNTVTAHI-----KKFTVCM-----ALSITLCFVFMW----- 344  
Db 271 FLLQMOENWVAYANHOEIPHIINNAFKOTFANVGGSGNTIGLLIAIFIGKQKQYKDIS 330  
QY 345 ----TP---NVSEKILIDIIGVDFAFELCVPLRIFSPFPVTVRAHLTGWL--MTLK 395  
Db 331 KLSAAPSLENISEPI---IFGLPIVFNPLLIIPVLAPIESLTTAYVATAAGNINHVWVQ 387  
QY 396 KTFVLAP-----SSVLRIIVLIASL-VLPLYL 421  
Db 388 TPWTTPPIISGLATGDNWRASVLQVLIIVTVTFIYLPFL 427

RESULT 7  
B83988  
Proline transporter opuE [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: B83988  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: B83988  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-507 <STO>  
A:Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06425.1; GSPDB:GNOC  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: opuE  
C:Superfamily: proline carrier protein

Query Match 4.6%; Score 115; DB 2; Length 507;  
Best Local Similarity 21.1%; Pred. No. 0.13;  
Matches 115; Conservative 75; Mismatches 186; Indels 168; Gaps 25;  
QY 45 AVELASVGLAYSLMKFTGP-----MSDF-----KN-----VGLFVNSKRDRTKAVLCM 90  
Db 8 AVAILIYVALLIGLLSSKSSVGMVTFIAGRNKNTVALSAVSSGR-----SAWLVL 64  
QY 91 VVAG-----AJAAVFHTLIAYSDLYIINKLHHVDESVS-----KTR----- 129  
Db 65 GWTGTAVATGLDAVAVAGYITVEVFLFFVARRFRAYSQTGSIITPIDILETRFNDKTH 124  
QY 130 -----RAFL-----YLAAF-----PFMDAMA-----WTHAGILLKHKYSFLVYCA 164  
Db 125 ILRGSAFIIMFFMIAYVASOLVAGGAFATSMGVSSSTGMWTVAVILL--AVTMLGGFH 182  
QY 165 SIS--DVI--AQGVFVAILLHSHLCREPLIPIILSLY-----VILPVAIIGLGGFDLQVMHTEGGFTSPF 198  
Db 183 AVSKTDVVOAGFMFVSL-----VILPVAIIGLGGFDLQVMHTEGGFTSPF 231  
QY 199 ---MGALVRCITCLGYGKNIHDIIPDSGPELGGDATIRKMLSF-----WPLALILAT 250  
Db 232 AFGGAVGTLGIGGSPGNPHILVRYNSLKNVKNEMQAALISSVMNVLGMGAVMTGLA 291  
QY 251 ORISRPVNLVFSRDLGGSSAATEAVAILTATVPVGMPLTEIRAVYPAFDKNNPSN 310  
Db 292 GRAYFPDVLSPNGD-----QEQVFLMGLSEILHPLFFGFL--LVAVLAAMSSADSQ 342  
QY 311 KLVSNTNTVTAHIKKF-----TFVCMALSLTLCFV-----MFTWPNV 348  
Db 343 LLVGSSAFVRIYQRMFRNRKLSOKKLVRSLRLTIVVFMGLSLILAFTAQEFVFWN--- 399

QY 349 SEKILIDIIGVDFAFEL--CVVPLRIFSPFPVTVRAHLTGWLMTLKKTFVL--APSS 404  
Db 400 -----VLFAFGGLGACFGPALLLSFYKWKVTRQGVLMGMIAGLLFVLVKKQPOW 449  
QY 405 VLRIIVLIASLVLPYLGVHGATLGVGSLAGFYGESTMVAIAACYVYR-----KQKKQME 460  
Db 450 TYARLPDVKELLNTVFFGI-----TVEAVPGFIVATTITVVISLTKRPHAKQIIERL 503  
QY 461 NESA 464  
Db 504 NESA 507

RESULT 8  
F69433  
conserved hypothetical protein AF1471 - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 08-Oct-1999  
C:Accession: F69433  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
A:Reference number: A69250; MUID:98049343; PMID:9389475  
A:Accession: F69433  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-447 <KLE>  
A:Cross-references: GB:AB001001; GB:AB000782; NID:g2689324; PIDN:AAB89777.1; PID:g26490;  
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0709

Query Match 4.5%; Score 114.5; DB 2; Length 447;  
Best Local Similarity 21.1%; Pred. No. 0.12;  
Matches 97; Conservative 78; Mismatches 164; Indels 121; Gaps 24;  
QY 19 PLGITNIAIDEG-----EQALNRGIAAVKEDAVEMLASVGLAYSIMKPFPTGMSDFKNVG 73  
Db 56 PIFFVFIASIFGLSVGANSVSRRIKARYAACVAATLAVANGIL--VSIPMT-----LS 109  
QY 74 LVFVNSKRDRTKAVLCMVVAGIAAVFHTLIAYSDLYIINKLHHVDES-----GSK 127  
Db 110 VVFLNG-----VWVFLGADGGEILRLAVDYGSI--MWLGSVFLVPSNVSAGILNGEG 158  
QY 128 TRAPLYLAAPFPMDAMAWTAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLECR 187  
Db 159 NARMAYANA-----AGSLINMVLDPIFYLLGYGIAGAAIASVISMAL----- 202  
QY 188 EPLLIPILSLYMGALVRCITCLGYGKNIHDIIPDSGPELGGDATIRKMLSF----- 241  
Db 203 -----SSIVFSW-----FLSGRSYVAFRVAGNMLPTVF 231  
QY 242 -----WPLALILATORISRPVNLVFSRDLGGSSAATEAVAILTATVPV---GHMP-YG 291  
Db 232 DLRLVGMFASLSMLTMSVAFMLINRWVI--ETGGS-----EGLAAYTSAWRLIQFGFVPLFG 286  
QY 292 WLTEIRAVY--PAFDKNNPSNKLVSNTVTAHIKKFTFVCMALSLTLCFVFMFTWPNV 350  
Db 287 VSAALTAVSAGAYGARNPRKIGESLNTV-----KLILAVDAAI--LALVAFAPQIA- 337  
QY 351 KILIDIIGVDFAFELCVVPLRIFSPF-----PVPVTVRAHLTGWLMTLKKTFVLAPSSVL 406  
Db 338 -LIFTYTEVSATVMEIEIVRTIRIAAFVLLFAPLGVSSSAVFQG-MGKERSFAI---TVL 392  
QY 407 RIIVLIASL---VLPYLGVHGATLG--VGSILAGFVGES 441  
Db 393 RAIVFQVSLCYLVAVFP--GFDGVLGFLVGLGALGCTGFS 431

RESULT 9  
E89978

high affinity proline permease [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
C:Accession: E89978  
R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguda, A.; Mizutani-Tai, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Ma, A.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
A:Reference number: A89758; MUID:21311952; PMID:11418146  
A:Accession: E89978  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-512 <CUR>  
A:Cross-references: CB:BA000018; PID:g13701695; PIDN:BA842988.1; GSPDB:GN00149  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: putP  
C:Superfamily: proline carrier protein

Query Match 4.5% Score 113.5; DB 2; Length 512;  
Best Local Similarity 18.8%; Pred. No. 0.17; Indels 173; Gaps 17;  
Matches 90; Conservative 66; Mismatches 149; Indels 173; Gaps 17;

QY 53 GLAYSLMKFTGPMSPDKFNVGLVFVNSKRDRTKAVLCQWVAGAAIAVFTHTLIAYSDLGYY 112  
DB 117 GDAITLPDFKFNLRDNKNV-----LKIISGLIIVVFFTL--YTHSGPV 158  
QY 113 IINKLHVDESVGSKTRAFELYLAAPFPMAMANTHAGILLKHKYSFLVG--CASISDVI 170  
DB 159 SGGKLF--ESAFGLDYHFGLLVAF-----IVIFYTFPGGYLAVSITDFF 201  
QY 171 AQVVFVAILLHSHLDECEPLIPI-----LSLXWVG--ALVR 204  
DB 202 QGVIMLTAM-----VWVPVIVAMNVLNGCTFHDVAMKPTNLNLPKGLSFGIIS 251  
QY 205 CTTLCGLGYKNIHDIIPRSGPELGGDATIRKMLSFWWPLAL----- 246  
DB 252 LFSWGLGYGQPHIIVRFMSIKSHKMLPKARRLGISWVAVGLLGAVAGLTGIAFPAYH 311  
QY 247 -----ILATORISRPVNLVRSRDILGGSSAATEAVAAILTATVPVGHMFPVGNLTET 296  
DB 312 IKLEDPTEPLFVMSQVLFHPLV-----GGFLLAAILAAIMSTI----- 349  
QY 297 RAVYPAPDKNPNKSLVSTGNTVT-----AAHIKPTFFVCMALSITLCFV-- 341  
DB 350 -----SQQLVTSSTLDFVFKLIRGEKAKTKQKPFVMIGRSLVSLVAIVAI 397  
QY 342 -MFWTPNVSEKILIDIGVDFAPFAELCWPLRIFSPFPVPTVRAHTGMLTKKTFTVL 400  
DB 398 AIAWNPN--DTILNLVGNWAGFGSFLPLVFALYWKGLTRAGAVSGMV----- 445  
QY 401 APSVLAIRIIVLIASLWPLVPLGVGHGATLGVSLHAGFVGSESTMVAIAACVYRKQKK 458  
DB 446 --SCALVVIVVIAWIKPLAHI---NEIFGLYEIIPGI-----VSVIVTVVSKLTAK 493

RESULT 10  
S02154  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Podospora anserina mitochondrion  
N:Alternate names: NADH-ubiquinone oxidoreductase chain 2  
C:Species: mitochondrion Podospora anserina  
C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 03-Jun-2002  
C:Accession: S02154  
R:Cummings, D.J.; Domenico, J.M.  
J. Mol. Biol. 204, 815-839, 1988  
A:Title: Sequence analysis of mitochondrial DNA from *Podospora anserina*.  
A:Reference number: S02153; MUID:89125610; PMID:2975708  
A:Accession: S02154  
A:Molecule type: DNA  
A:Residues: 1-556 <CUR>  
A:Cross-references: EMBL:X14485; NID:g13296; PIDN:CAA32646.1; PID:g13297  
C:Genetics:



QY 3 KFPALHY-W-----PLIRFLVPLGITNIAIDFQEQALNRGIAAIVKEDAVEMLASVGLAYS 57  
Db 31 KTLMAQYHNDPATPALAFSINMGIIIPLMITWGRMDNG-----KGQAIIVIGGILFS 84  
QY 58 L-----MKFTGPMSPDKVNGLVFVNSKR-----DRTKAVLCWVAGIAIA 98  
Db 85 LGFILSGFVNPLMLFUTYGVIAGLGSLAFTGNLNNILKFFPDRGLASGIVLAGVG 144  
QY 99 VFHTLIAYSDIGYYIINKLHHVDSVSGSKTRRAFLYLAAPFFMDAMATHAGILLKHYS 158  
Db 145 ---TLLC-TRLAIFYMAQTHDVS-----RALLYLG----- 170  
QY 159 FLVGCASISDVIAQVFAVAILLHSHLSREPLLIPIILSLYMGALVRCITLCLGYKNIHD 218  
Db 171 -----IVLVVIF-----IVQFFI----- 184  
QY 219 IIPDRSGP-BLGG-----DATIRKMLS-FWFLALILATORISPIVNLVSRDLG- 267  
Db 185 ---RSAPAKDSGGIKASPLDKDYRHLKDLRFLWLLFMILALGVFSQMWIS-SSAQIGM 239  
QY 268 ---GSSAATEAVAILTATYPVGHMPYGNLFEIRAVYAFDKNPNKLVSTSNVTAHI 324  
Db 240 TQYGLLSGALVSVLSFNSIGRLFWGLTDLKGGY-----NTLVIVYL 283  
QY 325 KKFTFVCVALSILTLCFVMFNPVNSEKILIDIIIGVDFAFACLVVPLRI----- 373  
Db 284 ---FICVCMLL-----LFFNGNTS-VYFESALGVGFAYAGILVIFGLTSQNFGRNQ 334  
QY 374 ---PSFF-----PVPTVTRAHTLGMWLTUKTFVLAPSSVLRILVILASLVLPY 420  
Db 335 LNYGMYEGFAVAGIAPVYTSIAKYTGSYNTV---FIL---TTVLLIGVVTULTIKKY 389  
QY 421 L 421  
Db 390 V 390  
RESULT 12  
T48676  
proline uptake protein [validated] - Staphylococcus aureus  
C:Species: Staphylococcus aureus  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 21-Jul-2000  
C:Accession: T48676  
R:Schwan, W.R.; Coulter, S.N.; Ng, E.Y.; Langhorne, M.H.; Ritchie, L.L.; We  
Infect. Immun. 66, 567-572, 1998  
A:Title: Identification and characterization of the PutP proline permease that contribut  
A:Reference number: 224528; MUID:98114355; PMID:9453610  
A:Accession: T48676  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-497 <SCCH>  
A:Cross-references: EMBL:AF024571; NID:92565310; PIDN:AAC38087.1; PID:92565311  
A:Experimental source: strain RN6390  
C:Genetics:  
A:Gene: putP  
C:Function:  
A:Description: involved in proline uptake [validated, MUID:98114355]  
C:Superfamily: proline carrier protein  
C:Keywords: amino acid transport; proline transport; transmembrane protein  
Query Match 4.5%; Score 112.5; DB 2; Length 497;  
Best Local Similarity 18.8%; Pred. No. 0.2;  
Matches 90; Conservative 66; Mismatches 149; Indels 173; Gaps 17;  
QY 53 GLAYSLMKFTGPMSPDKVNGLVFVNSKDRYKAVLCWVAGIAAIVPHTLIAYSDIGYY 112  
Db 116 GDAITLPDFFQKRLNDKNNV-----LKIISGLIIVVFTTL--YTHSGFV 157  
QY 113 IINKLHHVDSVSGSKTRRAFLYLAAPFFMDAMATHAGILLKHYSFVLG--CASISDVI 170  
Db 158 SGKLPF---ESAFGLDYHGLILVAF-----IVIFYFFGGYLAIVSITDFF 200

QY 171 AQVFAVAILLHSHLECREPLLIPI-----LSLYMG-----ALVR 204  
Db 201 QGVIMLIAM-----VMPPIVAMNUNGWGTTFHDVAMKPTNUNLFLGSLFIIS 250  
QY 205 CTTCLCYGKNIHDIIPDRSGPELGGDATIRKMLSFWPLAL----- 246  
Db 251 LFSNGLGVFGQPHIIVRFMSIKSHKMLPKAARLGISWMAVGLLGAVAVGLTGIATFVPAYH 310  
QY 247 -----ILATQRTSRPIVNLVSRDLGSSAAATEAVAILTATYPVGHMPYGNLTEI 296  
Db 311 IKLEDPETLFVMSQVLFHPLV-----GGFLLAAILAAMSTI----- 348  
QY 297 RAVYPAFDKPNPNKLVSTSNVT-----AAHIKFTFVCMAISLTLCFV- 341  
Db 349 -----SSQLVTSLSLTFEDFYKLIRGBEAKTHQKEFVMIGRLSVLVVAIVAI 396  
QY 342 -MFWTPNVSEKILIDIIIGVDFAFACLVVPLRIISFPFVPTVTRAHTLGMWLTLLKTEVL 400  
Db 397 ATAMNPN---DTILNLVGNWAGFGASPLVLFALYWKGLTRAGAVSGMW- 444  
QY 401 APSVLIIRIIVIASLWPLVGLVGHGATLGVGLAGFVGBESTWVAIAACYVYRKQKK 458  
Db 445 --SGALVIVVIAWIKPLAHI---NEIFGLYEIIPGFI-----VSVIVTVVVSUKLTKK 492  
RESULT 13  
E69609  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Bacillus subtilis  
N:Alternate names: caa3-605 cytochrome-c oxidase chain I; cytochrome-aa3 chain I  
C:Species: Bacillus subtilis  
C>Date: 03-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
C:Accession: E69609; S14397  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte;  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F  
Kotter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyana  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: E69609  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-622 <KUN>  
A:Cross-references: GB:Z99111; GB:AL009126; NID:92633699; PIDN:CAB13363.1; PID:92633661  
A:Experimental source: strain 168  
R:Saraate, M.; Metsco, T.; Nakari, T.; Jalli, T.; Laureus, M.; van der Oost, J.  
Eur. J. Biochem. 195, 517-525, 1991  
A:Title: The Bacillus subtilis cytochrome-c oxidase. Variations on a conserved protein  
A:Reference number: S14395; MUID:91146590; PMID:1847686  
A:Accession: S14397  
A:Molecule type: DNA  
A:Residues: 1-119, 'G', 121-154, 'SI', 157-287, 289-473, 'R', 475-622 <SAR>  
A:Cross-references: EMBL:X54140; NID:9994793; PIDN:CAA38077.1; PID:939870  
A:Experimental source: strain W168  
C:Genetics:  
A:Gene: ctad  
C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology  
C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-a  
F:23-467/Domain: cytochrome-c oxidase chain I homology <COI>  
F:27-43/Domain: transmembrane #status predicted <TM1>  
F:78-94/Domain: transmembrane #status predicted <TM2>  
F:107-123/Domain: transmembrane #status predicted <TM3>  
F:161-177/Domain: transmembrane #status predicted <TM4>  
F:203-219/Domain: transmembrane #status predicted <TM5>

Matches	95;	Conservative	68;	Mismatches	140;	Indels	133;	Gaps	22;
Qy	55	AYSIMKFTGPMGSDKFNVLGVFV--NSKRDRTKAVLCMVVAGAAIAVFTLLI-----AYS	107						
Db	61	AYILFAFPVQGIADSAFAKGRVMVANGKLGAAGICL--GVNPFVGYTLVGIGAAAYS	117						
Qy	108	DLGYIINKLHHVDESGSKTRAEFLAAFPFMDAMWTHAGILLK--HKYSLVGC-	164						
Db	118	PAKYGILGEL-----TTGDKLVKANGLMEASTAAILLGSVAGGVLADEWHVIAALVACAL	172						
Qy	165	SISDVIAQVVFVAILLHSHLECREPLILPILSLVMGALVR---CTTLCGLGYKN---IHD	218						
Db	173	AYAGAVAAFLFIPKLVAAR-----PGQSWRLSANTRSFFCA--CVVLRNGETRFS	221						
Qy	219	IIPDRSGPELGGDATIRKMLSEFMWPLALILATORISRPVNLFVSRLD--GSSSAATSAVA	277						
Db	222	LV--GTGLFGWAGVTLLFLLVWVPAVGLI--TDNATYTLNAMVAVGIVVAGAGAAKLVT	278						
Qy	278	ILTATYPVGHMYPYQWLTEI-----RAYVPADFKNPNPNKLVSTSTNTVTAHIKKFTF	329						
Db	279	LETVS---RCMPAGILIGVVAIFSLQHALLPAY-----	309						
Qy	330	VCMAISLTLCFVMFTWPNVSEKILIDIIIGVDFAEFLCVVPLRIFSFPVPVTVRAHLTG	389						
Db	310	---ALL-----LIGMLG-----GFFVFPENALLQBERG	334						
Qy	390	WLMTLKTF-----VLAPSSVLRIIVLIASLVVLVLYGVHGATLGVGSLLAGFVGE	440						
Db	335	-----KKSVGAGNAIAQVNLGENSEAMLLGLGLSLAVL--VGVPAAVIGIG-----FGV	381						
Qy	441	STMVAIAACYVYRKQK	456						
Db	392	LFALAAALWQRRQ	397						

RESULT 15

ABI437

PRPS system, cellobiose-specific IIC component homolog lin0033 [imported] - Listeria inno

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001

C:Accession: ABI437

D.; Dominguez-Bernal, G.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Ma

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: ABI437

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-452 <GLA>

A:Cross-references: GB:AL592022; PIDN:CA095266.1; PID:g16412454; GSPDB:GN00178

A:Experimental source: strain Ciipl1262

C:Genetics:

A:Gene: lin0033

C:Superfamily: phosphotransferase system enzyme II factor II, phosphoenolpyruvate-depend

Query Match 4.4%; Score 110.5; DB 2; Length 452;

Best Local Similarity 18.5%; Pred. NO. 0.26;

Matches 92; Conservative 86; Mismatches 173; Indels 145; Gaps 23;

Qy 59 MKFPTGSDKFNVLGVFVNSKRDRTKAVLCMVVAGAAIAVFTLLIAYSIDLGYIINKLH 118 || Db | 15 | LSIFPAKSSQHHWAI-----RDFAMIPITIAAFLLVNNVLLQPENG--LLKFTIP | 67 |
Qy	119	HYDESVG-----SKTRAEFLVLAAPPFMDAMWTHA-----GILLKHKGYFLVGCAS-	165
Db	68	NVENYLVGVQVYNATLGIMAAFLIGNFLAKSYGMGRTEGMVAAYVVLIPASSH	127
Qy	166	ISDVIAQVVFVAILLHSHLECREPLILPILSLVMGALVRCITLCL-GYYKNTHDIIPDRS	224

Db	128	LMSYDCKAFBAGGYLTQEMTSTGMLAIIA----	SLVSITMLAKFSKSLKISMPESV	183
Qy	225	GPELGGDATIRKMLSFWMPLALILATQISRPVNLVSRDL-----	GGSSA	271
Db	184	PP-----ATAKSFNIIIPSFVLVSLAIIIEVLVSVFVMSIPEIIVKVQIPLVGGPQT	237	
Qy	272	ATEAVAILTATYPVGHNPYGNLFEIRAVYPAFDKNPNPKLVNSTS-----	316	
Db	238	LP---GILLYVFLAGFL---W---VFGIHGAFVLGAISGPFVLLTSLQONIDAVNAGTALP	288	
Qy	317	NTVTAAHIKKF-----TFVCMALSLTLCFVMEWTP-----	NVSEKILI	354
Db	289	NIVTQPELDAFVVMGGGTIIICLVIAI---FIASKRPDHRMVTKFGLIPIFNVSEPLM-	344	
Qy	355	DIIGVDPAFAELCVPLRIEFPFPVPTVTEAHLT---GNLMTLKKTFVLAP-----	402	
Db	345	--FGLPVVFNPIYGIPLVI---APLASTAMAYFATSWG---ISQTYILIPWVTPPVLSG	396	
Qy	403	-----SSVLRI-IVLIASLVWLPYLGVHGATLGVGSLLAGFVGESTMWAIACVYV	452	
Db	397	YLATGGDIRASIIQIAIIVVGTIIYDPFV-----	LVANRAYVLE	435
Qy	453	RKQKKXWENESATEGE	468	
Db	436	QKAAGNVEAETVTNGE	451	

Search completed: April 22, 2004, 13:58:28  
Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2004, 13:50:23 ; Search time 18 Seconds  
(without alignment)  
1423.251 Million cell updates/sec

Title: US-09-978-188A-7

Perfect score: 2527

Sequence: 1 MVKFPALTHWPLRLFLVPL.....TDMPTTEVTDIVEMREENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2527	100.0	492	1 ANKH HUMAN	Q9hjc11 homo sapien
2	2502	99.0	492	1 ANKH MOUSE	Q9jhc22 mus musculus
3	2489	98.5	492	1 ANKH RAT	P58366 rattus norv
4	2317	91.7	492	1 ANKH XENLA	P58367 xenopus lae
5	2158.5	85.4	501	1 ANKH BRARE	P58368 brachydanio
6	1528.5	60.5	355	1 ANKH TETNG	P58369 tetraodon n
7	114	4.5	416	1 LACY KLEOX	P18817 klebsiella
8	113.5	4.5	556	1 PT2A PODAN	P15578 podospira a
9	111	4.4	622	1 COX1 BACSU	P24010 bacillus su
10	109.5	4.3	610	1 PT2A ARATH	P46031 arabidopsis
11	107	4.2	432	1 EXUT BACSU	O34456 bacillus su
12	107	4.2	533	1 LAT2 RAT	Q9wvr6 rattus norv
13	106	4.2	334	1 YB77 METJA	Q58578 methanococc
14	105	4.2	401	1 LSG1 HAEIN	P71399 haemophilus
15	105	4.2	676	1 HPPI METAC	Q8tja9 methanosarc
16	103.5	4.1	398	1 BCR HAEIN	P45123 haemophilus
17	103	4.1	417	1 LACY ECOLI	P02920 escherichia
18	102.5	4.1	446	1 CITN SALTY	P31604 salmonella
19	102.5	4.1	531	1 LAT2 MOUSE	Q9gxw9 mus musculus
20	102.5	4.1	533	1 NUSM RHITR	C05467 rhizobium t
21	102.5	4.1	641	1 NUSM ALIMA	P03365 allomyces m
22	101.5	4.0	446	1 CITN SALDU	P31603 salmonella
23	100	4.0	982	1 YS96 CAELU	Q09965 caenorhabdi
24	99	3.9	385	1 Y421 METTH	O26521 methanobact
25	99	3.9	535	1 LAT2 HUMAN	Q9ubi5 homo sapien
26	98.5	3.9	533	1 NU2M NUOCR	Q35140 neurospora
27	98.5	3.9	946	1 YB76 YEAST	P38250 saccharomyc
28	98	3.9	480	1 YEHA YEAST	P39981 saccharomyc
29	98	3.9	532	1 YABM BACSU	P37555 bacillus su
30	97.5	3.9	346	1 FMLR PONPY	P79235 pongo pygma
31	97.5	3.9	3803	1 TRAI DROME	Q818u7 drosophila
32	97	3.8	402	1 YYCB BACSU	P37482 bacillus su
33	96.5	3.8	346	1 FMLR_GORGO	P79176 gorilla gor

ALIGNMENTS

RESULT 1

ANKH\_HUMAN

ID ANKH\_HUMAN STANDARD; PRT; 492 AA.

AC Q9HCJ1; Q9NOW2;

DT 28-PEB-2003 (Rel. 41, Created)

DT 28-PEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Progressive ankylosis protein homolog (ANK).

GN ANKH OR KIAA1581.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_taxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20355194; PubMed=10894769;

RA Ho A.M., Johnson M.D., Kingsley D.M.;

RT "Role of the mouse ank gene in control of tissue calcification and

RT arthritis.";

RL Science 289:265-270(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=20450683; PubMed=10997877;

RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes.

RT XVIII. The complete sequences of 100 new cDNA clones from brain which

RT code for large proteins in vitro.";

RL DNA Res. 7:273-281(2000).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=22388257; PubMed=12477932;

RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]

RP VARIANTS CMDJ SER-375 DEL; PHE-376 DEL AND ALA-380 INS.

RX MEDLINE=21313103; PubMed=11326338;

RA Reichenberger E., Tiziani V., Watanabe S., Park L., Ueki Y.,  
RA Santana C., Baur S.T., Shiang R., Grange D.K., Beighton P.,  
RA Gardner J., Hamersma H., Sellars S., Ramesar R., Lidral A.C.,  
RA Sommer A., Raposo do Amaral C.M., Gorlin R.J., Mulliken J.B.,  
RA Olsen B.R.;  
RT "Autosomal dominant craniofacial dysplasia is caused by mutations  
RT in the transmembrane protein ANK";  
RL Am. J. Hum. Genet. 68:1321-1326(2001).  
RN [5];  
RP VARIANTS CMDJ ARG-292; ARG-331; SER-375 DEL; PHE-377 DEL; ALA-380 INS  
RP AND ARG-389.  
RX MEDLINE=2125282; PubMed=11326272;  
RA Nuernberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,  
RA Ritter H., Leschik G., Uhlmann K., Mischung C., Hartop K.,  
RA Goldblatt J., Borochowitz Z.U., Kotzot D., Westermann F., Mundlos S.,  
RA Braun H.-S., Laing N., Tinschert S.;  
RT "Heterozygous mutations in ANKH, the human ortholog of the mouse  
RT progressive ankylosis gene, result in craniofacial dysplasia";  
RL Nat. Genet. 28:37-41(2001).  
CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic  
CC pyrophosphate (PPi), probably functioning as ppi transporter.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
CC -!- TISSUE SPECIFICITY: Found in osteoblasts from mandibular bone and  
CC from iliac bone; not detected in osteoclastic cells.  
CC -!- DISEASE: Defects in ANKH are the cause of craniofacial dysplasia  
CC dysplasia Jackson type (CMDJ) [MIM:123000]. CMDJ is a rare  
CC autosomal dominant skeletal disorder characterized by abnormal  
CC bone formation and mineralization in membranous as well as  
CC endochondral bones. Progressive thickening of the bones can cause  
CC narrowing of cranial foramina and can lead to severe visual and  
CC neurological impairment, such as facial palsy and deafness.  
CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF274753; AAF88039.1; -;  
CC EMBL; AB046801; BAB13407.1; ALT\_INIT.  
CC EMBL; BC009835; AAH09835.1; -;  
CC EMBL; BC014526; AAH14526.1; -;  
CC Genew; HGNC:15492; ANKH.  
CC MIM; 605145; -;  
CC MIM; 123000; -;  
CC GO; GO:0016021; C:integral to membrane; IDA.  
CC GO; GO:0019867; C:outer membrane; TAS.  
CC GO; GO:0030504; F:inorganic diphosphate transporter activity; IDA.  
CC GO; GO:0005315; F:inorganic phosphate transporter activity; IDA.  
CC GO; GO:0007626; P:locomotory behavior; NAS.  
CC GO; GO:0030500; P:regulation of bone mineralization; TAS.  
CC GO; GO:0001501; P:skeletal development; NAS.  
CC Transport; Phosphate transport; Transmembrane; Disease mutation;  
CC Deafness.  
FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 86 106 POTENTIAL.  
FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 132 152 POTENTIAL.  
FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 159 179 POTENTIAL.  
FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 190 210 POTENTIAL.  
FT DOMAIN 211 326 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 327 347 POTENTIAL.  
FT DOMAIN 348 350 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 351 371 POTENTIAL.  
FT DOMAIN 372 403 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 404 426 POTENTIAL.  
FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 430 452 POTENTIAL.

FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).  
FT VARIANT 292 W -> R (in CMDJ).  
FT 331 /FTid=VAR\_012192.  
FT 331 C -> R (in CMDJ).  
FT 331 /FTid=VAR\_012193.  
FT 375 Missing (in CMDJ).  
FT 375 /FTid=VAR\_012194.  
FT 376 Missing (in CMDJ).  
FT 376 /FTid=VAR\_012195.  
FT 377 Missing (in CMDJ).  
FT 377 /FTid=VAR\_012196.  
FT 380 P -> PA (in CMDJ).  
FT 389 /FTid=VAR\_012197.  
FT 389 G -> R (in CMDJ).  
FT 78 /FTid=VAR\_012198.  
FT 78 N -> S (in REF. 1).  
SQ CONFLICT 78  
SQ SEQUENCE 492 AA; 54240 MW; 44BFE9089BDEC6B CRC64;  
  
Query Match 100.0%; Score 2527; DB 1; Length 492;  
Best Local Similarity 100.0%; Pred. No. 7.8e-195; Indels 0; Gaps 0;  
Matches 492; Conservative 0; Mismatches 0;  
  
QY 1 MVKFPALTHYWLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
DB 1 MVKFPALTHYWLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
QY 61 FTGPMSPDNVGLVFNKSRDRTKAVLCMVVAGIAAVFHTLIAYSDLYGIYINKLHV 120  
DB 61 FTGPMSPDNVGLVFNKSRDRTKAVLCMVVAGIAAVFHTLIAYSDLYGIYINKLHV 120  
QY 121 DESVGSKTRAFLYLAAPFFMDAMANTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
DB 121 DESVGSKTRAFLYLAAPFFMDAMANTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
QY 181 HSHLECREPLLIISLYNGALVRCITCLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240  
DB 181 HSHLECREPLLIISLYNGALVRCITCLGYKNIHDIIPDRSGPELGGDATIRKMLSF 240  
QY 241 WPLALILATQIRISPIVNLVSRDLGGSSAATEAVAILTATVPYGHMPYGLTIRAVY 300  
DB 241 WPLALILATQIRISPIVNLVSRDLGGSSAATEAVAILTATVPYGHMPYGLTIRAVY 300  
QY 301 PAFDKNPNKLVSTNTVTAHKKFTFVCMALSLTLCFVNFVTPNVSEKILIDIIIGVD 360  
DB 301 PAFDKNPNKLVSTNTVTAHKKFTFVCMALSLTLCFVNFVTPNVSEKILIDIIIGVD 360  
QY 361 FAFAEICVVPRLRIFSPFPVTVRAHLTGMLTKTKTFLVAPSSVLRITVLIASLVLPY 420  
DB 361 FAFAEICVVPRLRIFSPFPVTVRAHLTGMLTKTKTFLVAPSSVLRITVLIASLVLPY 420  
QY 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRKQKKQKNESATEGEDSAMTMPPTTE 480  
DB 421 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRKQKKQKNESATEGEDSAMTMPPTTE 480  
QY 481 VTDIVEMRENE 492  
DB 481 VTDIVEMRENE 492  
  
RESULT 2  
ANKH\_MOUSE  
ID ANKH\_MOUSE STANDARD; PRT; 492 AA.  
AC Q9UHZ2; O35138; O35139;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Progressive ankylosis protein (Fn54 protein).  
GN ANKH OR ANK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

SEQUENCE FROM N.A., AND VARIANT VAL-201.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=20355194; PubMed=10894769;  
 RA Ho A.M.; Johnson M.D.; Kingsley D.M.;  
 RT "Role of the mouse ank gene in control of tissue calcification and  
 RL arthritis.";  
 RN Science 289:265-270 (2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Guo Y.; Hsu D.K.W.; Alberts G.F.; Feng S.-L.; Copeland N.G.;  
 RA Gilbert D.J.; Jenkins N.A.; Peiffley K.A.; Winkles J.A.;  
 RT "Molecular cloning and characterization of a mitogen-inducible gene  
 RT differentially expressed in androgen-dependent and independent  
 RT prostate carcinoma cell lines.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic  
 CC pyrophosphate (Ppi), probably functioning as Ppi transporter.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -!- TISSUE SPECIFICITY: Expressed in heart, brain, liver, spleen,  
 CC lung, muscle, and kidney of adult animals. Strongly expressed in  
 CC the developing articular cartilage of joints in the shoulder,  
 CC elbow, wrist, and digits of the embryo.  
 CC -!- DISEASE: Defects in ANKH are the cause of a generalized,  
 CC progressive form of arthritis. In ank mice hydroxyapatite crystals  
 CC develop in articular surfaces and synovial fluid leading to joint  
 CC space narrowing, cartilage erosion, and formation of bony  
 CC outgrowths or osteophytes that cause fusion and joint immobility  
 CC and destruction.  
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.  
 CC  
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 CC  
 DR EMBL; AF274752; AAF88038.1; -;  
 DR EMBL; AF001532; AAB65653.1; -;  
 DR EMBL; AF001533; AAB65654.2; -;  
 DR MGD; MGI:88023; ank.  
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.  
 DR GO; GO:0019867; C:outer membrane; IEA.  
 DR GO; GO:0030504; P:inorganic diphosphate transporter activity; IDA.  
 DR GO; GO:0007626; P:locomotory behavior; IMP.  
 DR GO; GO:0003050; P:regulation of bone mineralization; IMP.  
 DR GO; GO:0001501; P:skeletal development; IMP.  
 KW Transport; Phosphate transport; Transmembrane; Polymorphism.  
 FT DOMAIN 1 85  
 FT DOMAIN 86 106  
 FT TRANSMEM 107 131  
 FT DOMAIN 132 152  
 FT TRANSMEM 153 158  
 FT DOMAIN 159 179  
 FT TRANSMEM 180 189  
 FT DOMAIN 190 210  
 FT TRANSMEM 211 326  
 FT DOMAIN 327 347  
 FT TRANSMEM 348 350  
 FT DOMAIN 351 371  
 FT TRANSMEM 372 403  
 FT DOMAIN 404 426  
 FT TRANSMEM 427 429  
 FT DOMAIN 430 452  
 FT TRANSMEM 453 452  
 FT VARIANT 201 201 A -> V (IN STRAIN C3H).  
 SQ SEQUENCE 492 AA; 54297 MW; 8792B248C875688E CRC64;  
 Query Match 99.0%; Score 2502; DB 1; Length 492;  
 Best Local Similarity 98.4%; Pred. No. 7,9e-193;  
 Matches 484; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

1 MYKFPALTHYPLIRFLVPLGTTNIAIDFGQALNRGIAAVKEDAVEMLASGLAYSLMK 60  
 1 MYKFPALTHYPLIRFLVPLGTTNIAIDFGQALNRGIAAVKEDAVEMLASGLAYSLMK 60  
 61 FTGPMSPFNKVLVFNKSKDRKAVLCMVVAGAAVAFHTLIAYSDGLYYINKLHHV 120  
 61 FTGPMSPFNKVLVFNKSKDRKAVLCMVVAGAAVAFHTLIAYSDGLYYINKLHHV 120  
 121 DESVSGKTRRAFLYLAAPFFMDAMANTHAGILLKHYSFLVGCASISDVIAQVFAILL 180  
 121 DESVSGKTRRAFLYLAAPFFMDAMANTHAGILLKHYSFLVGCASISDVIAQVFAILL 180  
 181 HSHLECREPLIPILSLYMGALVRCVTTCLGYKYNHDIIPDRSGPELGGDATIRKMLSF 240  
 181 HSHLECREPLIPILSLYMGALVRCVTTCLGYKYNHDIIPDRSGPELGGDATIRKMLSF 240  
 241 WPLALILATQIRISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGLWTEIRAVY 300  
 241 WPLALILATQIRISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGLWTEIRAVY 300  
 301 PAFDKNPNKSLVSTNTVTAAHIKKFTFCVMSLTLTLCFVNFMTPNVSEKILDIIGVD 360  
 301 PAFDKNPNKSLVSTNTVTAAHIKKFTFCVMSLTLTLCFVNFMTPNVSEKILDIIGVD 360  
 361 PAFDELCTVPLIFSFPPVPTVRAHLTCGLMTLTKTFLAPSSVLRILVLTASLVLPY 420  
 361 PAFDELCTVPLIFSFPPVPTVRAHLTCGLMTLTKTFLAPSSVLRILVLTASLVLPY 420  
 421 LGVHGATLGVSLAGFVGESTWVAIAACYVYRKQKKMENESATEGDSAMTDPPTTE 480  
 421 LGVHGATLGVSLAGFVGESTWVAIAACYVYRKQKKMENESATEGDSAMTDPPTTE 480  
 481 VTDIVEMREENE 492  
 481 VTDIVEMREENE 492

RESULT 3  
 ANKH RAT STANDARD; PRT; 492 AA.  
 AC P58366;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Progressive ankylosis protein homolog (ANK).  
 GN ANKH.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;  
 RA Miyashiro K.; Finnell R.H.; Eberwine J.;  
 RT "Rat progressive ankylosis gene/termesin.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic  
 CC pyrophosphate (Ppi), probably functioning as Ppi transporter (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Membrane protein (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.  
 CC  
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 CC  
 DR EMBL; AF393241; AAK73750.1; -;  
 DR GO; GO:0016021; C:integral to membrane; ISS.

DR GO:0019867; C:outer membrane; ISS.  
 DR GO:0030504; F:inorganic diphosphate transporter activity; ISS.  
 DR GO:0030500; P:regulation of bone mineralization; ISS.  
 KW Transport; Phosphate transport; Transmembrane.  
 FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 86 106 POTENTIAL.  
 FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 132 152 POTENTIAL.  
 FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 190 210 POTENTIAL.  
 FT DOMAIN 211 326 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 327 347 POTENTIAL.  
 FT DOMAIN 348 350 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 351 371 POTENTIAL.  
 FT DOMAIN 372 403 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 404 426 POTENTIAL.  
 FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 430 452 POTENTIAL.  
 FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 492 AA; 54264 MW; 99CAC276412ECOB CRC64;  
  
 Query Match 98.5%; Score 2489; DB 1; Length 492;  
 Best Local Similarity 97.8%; Pred. No. 8.6e-192;  
 Matches 481; Conservative 6; Mismatches 5; Indels 0; Gaps 0;  
  
 QY 1 MKVEPALTHWPLIRFLVPLGTTNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
 DB 1 MKVEPALTHWPLIRFLVPLGTTNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
  
 QY 61 FFTGPMDFKXNGVLVFNYSKRDRTKAVLCMVVAGIAAFTLTIAYSDLGYYIINKLHV 120  
 DB 61 FFTGPMDFKXNGVLVFNYSKRDRTKAVLCMVVAGIAAFTLTIAYSDLGYYIINKLHV 120  
  
 QY 121 DESVGSKTRRAFLVLAAPPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180  
 DB 121 DESVGSKTRRAFLVLAAPPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180  
  
 QY 181 HSHLECREPLIPILSYMGALVRCCTTLCGLYKNIHDIIPDRSGPELGGDATIRKMLSF 240  
 DB 181 HSHLECREPLIPILSYMGALVRCCTTLCGLYKNIHDIIPDRSGPELGGDATIRKMLSF 240  
  
 QY 241 WPLALILATORISRPVNLFSVLDGSSNAFAVAILTATVPVGHMPYCWLTETRAVY 300  
 DB 241 WPLALILATORISRPVNLFSVLDGSSNAFAVAILTATVPVGHMPYCWLTETRAVY 300  
  
 QY 301 PAFDKNPNKLVSTNTVTAAHIKKFTFCWALSLLTLCFVMEFTPNVSEKILIDIIGVD 360  
 DB 301 PAFDKNPNKLVSTNTVTAAHIKKFTFCWALSLLTLCFVMEFTPNVSEKILIDIIGVD 360  
  
 QY 361 FAPAEELCVPLIRISFPFVPTVRAHLTGWLTKTFFVLAPSSVLIILVILASLVLPY 420  
 DB 361 FAPAEELCVPLIRISFPFVPTVRAHLTGWLTKTFFVLAPSSVLIILVILASLVLPY 420  
  
 QY 421 LGVHGATLGVSLLAGFVGESTWVAIAACYVYRKQKKMENESATEGEDSANTDMPTEE 480  
 DB 421 LGVHGATLGVSLLAGFVGESTWVAIAACYVYRKQKKMENESATEGEDSANTDMPTEE 480  
  
 QY 481 VTDIVEMRENE 492  
 DB 481 VTDIVEMRENE 492  
  
 RESULT 4  
 ANKH\_XENLA  
 ID ANKH\_XENLA STANDARD; PRT; 492 AA.  
 AC P58367;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Progressive ankylosis protein homolog (ANK).  
 GN ANKH.

OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21225282; PubMed=11326272;  
 RA Nuenberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,  
 RA Ritter H., Leesch G., Uhlmann K., Mischung C., Harrop K., Mundlos S.,  
 RA Goldblatt J., Borochowitz Z.U., Kotzot D., Westermann F., Mundlos S.,  
 RA Braun H.-S., Laing N., Tinschert S.;  
 RT "Heterozygous mutations in ANKH, the human ortholog of the mouse  
 RT progressive ankylosis gene, result in craniometaphyseal dysplasia.";  
 RL Nat. Genet. 28:37-41(2001).  
 CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic  
 CC pyrophosphate (Ppi), probably functioning as Ppi transporter (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.  
 CC  
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 CC  
 CC EMBL: AJ302033; CAC40980.1; -;  
 DR GO:0016021; C:integral to membrane; ISS.  
 DR GO:0019867; C:outer membrane; ISS.  
 DR GO:0030504; F:inorganic diphosphate transporter activity; ISS.  
 DR GO:0030500; P:regulation of bone mineralization; ISS.  
 KW Transport; Phosphate transport; Transmembrane.  
 FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 86 106 POTENTIAL.  
 FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 132 152 POTENTIAL.  
 FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 159 179 POTENTIAL.  
 FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 190 210 POTENTIAL.  
 FT DOMAIN 211 327 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 328 348 POTENTIAL.  
 FT DOMAIN 349 360 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 361 381 POTENTIAL.  
 FT DOMAIN 382 403 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 404 426 POTENTIAL.  
 FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 430 452 POTENTIAL.  
 FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 492 AA; 53951 MW; 753214B87D7B5F23 CRC64;  
  
 Query Match 91.7%; Score 2317; DB 1; Length 492;  
 Best Local Similarity 90.2%; Pred. No. 5.1e-178;  
 Matches 444; Conservative 25; Mismatches 23; Indels 0; Gaps 0;  
  
 QY 1 MKVEPALTHWPLIRFLVPLGTTNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
 DB 1 MKVEPALTHWPLIRFLVPLGTTNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMK 60  
  
 QY 61 FFTGPMDFKXNGVLVFNYSKRDRTKAVLCMVVAGIAAFTLTIAYSDLGYYIINKLHV 120  
 DB 61 FFTGPMDFKXNGVLVFNYSKRDRTKAVLCMVVAGIAAFTLTIAYSDLGYYIINKLHV 120  
  
 QY 121 DESVGSKTRRAFLVLAAPPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180  
 DB 121 DESVGSKTRRAFLVLAAPPFMDAMWTHAGILLKHYSFLVGCASISDVIAQVFWVAILL 180  
  
 QY 181 HSHLECREPLIPILSYMGALVRCCTTLCGLYKNIHDIIPDRSGPELGGDATIRKMLSF 240  
 DB 181 HSHLECREPLIPILSYMGALVRCCTTLCGLYKNIHDIIPDRSGPELGGDATIRKMLSF 240

QY 241 WPLALILATORISRPVNLVFSRDLGGSSAATAEVAAILTATYPVGHMPYGLTEIRAVY 300  
 FT DOMAIN 211 327 POTENTIAL.  
 FT TRANSSEM 190 210 POTENTIAL.  
 DB 241 WPLALILATORISRPVNLVFSRDLGGSSAATAEVAAILTATYPVGHMPYGLTEIRAVY 300  
 FT TRANSSEM 328 348 POTENTIAL.  
 FT TRANSSEM 349 362 EXTRACELLULAR (POTENTIAL).  
 QY 301 PAFDKNPNKLVSTNTVTAHKKFTVCWALSILTLFCVNFMTPNVSEKILDIIGVB 360  
 FT TRANSSEM 384 403 POTENTIAL.  
 DB 301 PAFDKNPNKLVSTNTVTAHKKFTVCWALSILTLFCVNFMTPNVSEKILDIIGVB 360  
 FT TRANSSEM 404 426 POTENTIAL.  
 QY 361 PAFDELGVVPLRIFGFPVPTVRAHLTGWMLTKKTFVLAAPSSVLRIVLIIASVILPY 420  
 FT TRANSSEM 427 429 EXTRACELLULAR (POTENTIAL).  
 DB 361 PAFDELGVVPLRIFGFPVPTVRAHLTGWMLTKKTFVLAAPSSVLRIVLIIASVILPY 420  
 FT TRANSSEM 430 452 POTENTIAL.  
 QY 421 LGVHGATLGVSLLAGFVCESTWVAIAACVYVRKOKKKNESATEGEDSAMTDPTEE 480  
 FT TRANSSEM 453 501 POTENTIAL.  
 DB 421 LGVHGATLGVSLLAGFVCESTWVAIAACVYVRKOKKKNESATEGEDSAMTDPTEE 480  
 FT TRANSSEM 501 AA; 55415 MW; E2A4F6362871CB4 CRC64;  
 QY 481 VTDIVEMRENE 492  
 FT TRANSSEM 501 AA; 55415 MW; E2A4F6362871CB4 CRC64;  
 DB 481 LTDIVKEIDGE 492  
 FT TRANSSEM 501 AA; 55415 MW; E2A4F6362871CB4 CRC64;  
 RESULT 5  
 ANKH BRARE  
 ID ANKH BRARE STANDARD; PRT; 501 AA.  
 AC P58368;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Progressive ankylosis protein homolog (ANK).  
 GN ANKH.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP MEDLINE=21225282; PubMed=11326272;  
 RX Nuerberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,  
 RA Ritter H., Leschik G., Uhlmann K., Mischung C., Harrop K.,  
 RA Goldblatt J., Borochowitz Z.U., Korzot D., Westermann F., Mundlos S.,  
 RA Braun H.-S., Laing N., Tinschert S.;  
 RT "Heterozygous mutations in ANKH, the human ortholog of the mouse  
 progressive ankylosis gene, result in cranioetaphyseal dysplasia."  
 RL Nat. Genet. 28:37-41(2001).  
 CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic  
 pyrophosphate (PPi), probably functioning as Ppi transporter (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.  
 CC  
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 CC  
 CC ENBL; AJ302035; CAC40781.1;  
 DR GO:0016021; C:integral to membrane; ISS.  
 DR GO:0019857; C:outer membrane; ISS.  
 DR GO:0005315; F:inorganic phosphate transporter activity; ISS.  
 DR GO:0030500; P:regulation of bone mineralization; ISS.  
 KW Transport; Phosphate transport; Transmembrane.  
 FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 86 106 POTENTIAL.  
 FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 132 152 POTENTIAL.  
 FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 159 179 POTENTIAL.  
 FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 190 210 POTENTIAL.  
 FT DOMAIN 211 327 POTENTIAL.  
 FT TRANSSEM 328 348 POTENTIAL.  
 FT TRANSSEM 349 362 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 384 403 POTENTIAL.  
 FT TRANSSEM 404 426 POTENTIAL.  
 FT TRANSSEM 427 429 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 430 452 POTENTIAL.  
 FT TRANSSEM 453 501 POTENTIAL.  
 SQ SEQUENCE 501 AA; 55415 MW; E2A4F6362871CB4 CRC64;  
 Query Match 85.4%; Score 2158.5; DB 1; Length 501;  
 Best Local Similarity 83.0%; Pred. No. 2.5e-165;  
 Matches 411; Conservative 45; Mismatches 36; Indels 3; Gaps 2;  
 QY 1 MKPEPALTHWPLRIFLPLGINTIAIDFGEOALNRGIAAIVKEDAVEMLASGLAYSLMK 60  
 DB 1 MKPEPALTHWPLRIFLPLGINTIAIDFGEOALNRGIAAIVKEDAVEMLASGLAYSLMK 60  
 QY 61 FFTGPMSEDFKNVGLVFNVSKRDRTKAVLCMVVAGATAAVERHTLIAYSDLGYYIINKLHV 120  
 DB 61 FFTGPMSEDFKNVGLVFNVSKRDRTKAVLCMVVAGATAAVERHTLIAYSDLGYYIINKLHV 120  
 QY 121 DESVGSKTRRAFLYLAAPFPMDAMWATHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
 DB 121 DESVGSKTRRAFLYLAAPFPMDAMWATHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
 QY 181 HSHLECEPELIPILSLYMGALVRCCTLCIGYKYNHDIIPDRSGPGLGDATIRKMLSF 240  
 DB 181 HSHLECEPELIPILSLYMGALVRCCTLCIGYKYNHDIIPDRSGPGLGDATIRKMLSF 240  
 QY 241 WPLALILATORISRPVNLVFSRDLGGSSAATAEVAAILTATYPVGHMPYGLTEIRAVY 300  
 DB 241 WPLALILATORISRPVNLVFSRDLGGSSAATAEVAAILTATYPVGHMPYGLTEIRAVY 300  
 QY 301 PAFDKNPNKLVSTNTVTAHKKFTVCWALSILTLFCVNFMTPNVSEKILDIIGVB 360  
 DB 301 PAFDKNPNKLVSTNTVTAHKKFTVCWALSILTLFCVNFMTPNVSEKILDIIGVB 360  
 QY 361 PAFDELGVVPLRIFGFPVPTVRAHLTGWMLTKKTFVLAAPSSVLRIVLIIASVILPY 420  
 DB 361 PAFDELGVVPLRIFGFPVPTVRAHLTGWMLTKKTFVLAAPSSVLRIVLIIASVILPY 420  
 QY 421 LGVHGATLGVSLLAGFVCESTWVAIAACVYVRKOKKKNESATEGEDSAMTDPTEE 477  
 DB 421 LGVHGATLGVSLLAGFVCESTWVAIAACVYVRKOKKKNESATEGEDSAMTDPTEE 477  
 QY 478 TEEVTDIVEMRENE 492  
 DB 481 RGRWDDIVELREDE 495

## RESULT 6

ANKH TETNG  
 ID ANKH TETNG STANDARD; PRT; 355 AA.  
 AC P58369;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Progressive ankylosis protein homolog (ANK) (Fragment).  
 GN ANKH.  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle.  
 RX MEDLINE=21225282; PubMed=11326272;  
 RA Nuerberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,



RA Ritter H., Ieschik G., Uhlmann K., Mischung C., Harrop K.,  
RA Goldblatt J., Borochowitz Z.U., Kotzot D., Westermann F., Mundlos S.,  
RA Braun H.-S., Laing N., Tinschert S.;  
RT "Heterozygous mutations in ANKH, the human ortholog of the mouse  
RT progressive ankylosis gene, result in cranioetaphyseal dysplasia";  
RL Nat. Genet. 28:37-41(2001).  
CC -!- FUNCTION: Regulates intra- and extracellular levels of inorganic  
CC pyrophosphate (PPi), probably functioning as Ppi transporter (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE ANKH FAMILY.  
CC  
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CC  
CC EMBL; AJ302034; CAC40964.1; -; 39336 MW; 09A70DCFF80F1B5C CRC64;  
KW TRANSPORT; Phosphate transport; Transmembrane.  
FT NON TER 1 1  
FT TRANSMEM 20 40 POTENTIAL.  
FT TRANSMEM 66 86 POTENTIAL.  
FT TRANSMEM 93 113 POTENTIAL.  
FT TRANSMEM 124 144 POTENTIAL.  
FT TRANSMEM 260 280 POTENTIAL.  
FT TRANSMEM 296 316 POTENTIAL.  
FT TRANSMEM 331 351 POTENTIAL.  
FT NON TER 355 355  
SQ SEQUENCE 355 AA; 39336 MW; 09A70DCFF80F1B5C CRC64;

Query Match 60.5%; Score 1528.5; DB 1; Length 355;  
Best Local Similarity 82.0%; Pred. No. 4.7e-115;  
Matches 292; Conservative 31; Mismatches 32; Indels 1; Gaps 1;

QY 67 SDFKNGVLVFNVRKDRTRKAYLCMVVAGIAAFTLTIAYSDLGYYIINKLHVDES VGS 126  
Db 1 SDFKNGVLVFNVRKDRKAMFLIYTAGTAFVLIHIIAYTDLGYIINKLHVDES VGG 60

QY 127 KTRRAFLYLAAPPNDANAWTHAGILKHKYSLVGCASISDVIAQVFAILLHSHLEC 186  
Db 61 KTRKAFLLAAPPDLDAWIAHAGILKHKYSLVGCASISDVIAQVFAILLHSHLEC 120

QY 187 REPLIPILSYMGALVRCCTTLCGYKNIHDIIPDRSGPGLGDATIRKMLSFWWPLAL 246  
Db 121 AEPLIPILSYMGALVFAFTVGLGYCNIHDIIPDTSGLDVGGDATIRKMLSFWWPLAL 180

QY 247 ILATORISRPVNLVFSRDLGSSNATEAVAILTATYVGHMPYGLWTEIRAVYPADFN 306  
Db 181 ILATORISRPVNLVFSRDLGSSNATEAVAILTATYVGHMPYGLWTEIRAVYPADFN 240

QY 307 NPSNKLVSNTVTAHKKFTFCVCMALSLTLCFVMTNPNVSEKILIDIIIGVDFAFEL 366  
Db 241 NPSNK-INASSPVTKSHIKKFTFCCLALSMLCFVLTWTPHSEKILVDVIGVDYFAEL 299

QY 367 CVVPLRIISFPVPTVRAHLTGWMLTKKTFVLAPSSVLRITVLIASLVLPYLG 422  
Db 300 CVVPLRIISFPVPTVRAHLTAWLTKKTFVLAPSSVLRITVLIASLVLPYMG 355

OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=571;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=M5a1;  
RX MEDLINE=89050993; PubMed=3056524;  
RA McMorrow I., Chin D.T., Fiebig K., Pierce J.L., Wilson D.M.,  
RA Reeve E.C.R., Wilson T.H.;  
RT "The lactose carrier of Klebsiella pneumoniae M5a1; the physiology of  
RT transport and the nucleotide sequence of the lacy gene.";  
RL Biochim. Biophys. Acta 945:315-323(1988).  
CC -!- FUNCTION: RESPONSIBLE FOR TRANSPORT OF BETA-GALACTOSIDES INTO THE  
CC CELL, WITH THE CONCOMITANT IMPORT OF A PROTON (SYMPORT SYSTEM).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.  
CC -!- SIMILARITY: BELONGS TO THE LACY/RAPE FAMILY OF PERMEASES  
CC  
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CC  
CC EMBL; X14154; CAA32366.1; -;  
DR PIR; C24925; C24925.  
DR InterPro; IPR000576; Lacy\_symport.  
DR InterPro; IPR007114; MFS.  
DR Pfam; PF01306; Lacy\_symp. 1.  
DR PRINTS; PRO0174; LACYSYMPORT.  
DR TIGRFAMs; TIGR00882; 2A0105; 1.  
DR PROSITE; PS00896; LACY\_1; 1.  
DR PROSITE; PS00897; LACY\_2; 1.  
DR PROSITE; PS00850; MFS; 1.  
KW TRANSPORT; Sugar transport; Symport; Inner membrane; Transmembrane.  
FT DOMAIN 1 13  
FT TRANSMEM 14 34  
FT DOMAIN 35 50  
FT TRANSMEM 51 71  
FT DOMAIN 72 80  
FT TRANSMEM 81 101  
FT DOMAIN 102 107  
FT TRANSMEM 108 130  
FT DOMAIN 131 149  
FT TRANSMEM 150 170  
FT DOMAIN 171 172  
FT TRANSMEM 173 193  
FT DOMAIN 194 223  
FT TRANSMEM 224 244  
FT DOMAIN 245 267  
FT TRANSMEM 268 288  
FT DOMAIN 289 316  
FT TRANSMEM 317 319  
FT TRANSMEM 320 339  
FT DOMAIN 340 353  
FT TRANSMEM 354 374  
FT DOMAIN 375 384  
FT TRANSMEM 385 405  
FT DOMAIN 406 416  
SQ SEQUENCE 416 AA; A37DB8A4C38C467B CRC64;

Query Match 4.5%; Score 114; DB 1; Length 416;  
Best Local Similarity 22.7%; Pred. No. 0.099;  
Matches 95; Conservative 50; Mismatches 145; Indels 128; Gaps 22;

QY 132 FYLAAAPPMDAMW--THAGILKHKYSLVGCASISDVIAQVFAILLHSHLEC 186  
Db 26 FIMSAYFPFPF--VWLAENVHLTKTGTGIVFSCISLFAIFQVFGILSKLGRKLLW 83  
QY 187 REPLLI-----PIL--SLYMGALVRCCTTLCGYKNIHDIIPDRSGP----- 226  
Db 84 TITILLPAPPIFVPSFLQNNINAGALVG-----GVILGI--VFSSRSGAVEAYTE 135

Query Match 4.5%; Score 113.5; DB 1; Length 556;  
Best Local Similarity 19.5%; Pred. No. 0.15; Mismatches 141; Indels 169; Gaps 21;  
Matches 94; Conservative 78;

QY 227 -----ELG-----GDA-----TIRKMLSFWP--LALILATQIRSPIV 258  
DB 136 RVSANREFYKRVSGVGCWALCASITGIIFSDPNITFIASGFALILG-----V 187  
QY 259 NLFVSRDLGGSSAAT-----EAVAILTATYPVGHMPYCW-----LTERAVYPAFDK 305  
DB 188 LLWVKPSSNSAEVIDALGANRQAFNRATA--ELFRMPREWFGLIYVGVASVYDFDQ 246  
QY 306 N--NPSNKLVTSTNTVTAHHKKTFFVCMALSLTLCFVMTFNPVSEKI----- 352  
DB 247 QFANFFKGFSSPQSGT-----EVFGVTTGGELLNALIMFCAPAIINRIGAKNALLIAGL 302  
QY 353 --LIDIIIGVDFAFELCVVPLRIITFFFPVTVRAHLTGMLTKTFLVAPSSVLRII-- 409  
DB 303 IMSVRLGSSFATSVEVILKMLHMFELPL-----LVGTETKVISSAFKGLSATLFLIG 358  
QY 410 -----VLIASVLVLPY--LVHGTATLGVSLLAGFV-----GESTWVAIAA 448  
DB 359 FNLSKQLSSVLSAWVGMYDTGVFQAYLILGCTITSFTVISLFTLKGSKTLPLATA 416

RESULT 8  
NUZM\_PODAN  
ID NUZM\_PODAN STANDARD; PRT; 556 AA.  
AC P15578;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).  
GN ND2.  
OS Podospora anserina.  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.  
OX NCBI\_TaxID=5145;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S;  
RX MEDLINE=89125610; PubMed=2975708;  
RA Cummings D.J., Domenico J.M.;  
RT "Sequence analysis of mitochondrial DNA from Podospora anserina.  
RT Pervasiveness of a class I intron in three separate genes.";  
RL J. Mol. Biol. 204:815-839(1988).  
RN [2]  
RP COMPLETE GENOME.  
RC STRAIN=S;  
RX MEDLINE=90291512; PubMed=2357736;  
RA Cummings D.J., McNally K.L., Domenico J.M., Matsuura E.T.;  
RT "The complete DNA sequence of the mitochondrial genome of Podospora  
RT anserina.";  
RL Curr. Genet. 17:375-402(1990).  
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane.  
CC -!- SIMILARITY: Belongs to the complex I subunit 2 family.  
CC  
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CC  
CC EMBL; X55026; CAA38765.1; -;  
DR EMBL; X14485; CAA32646.1; -;  
DR PIR; S02154; S02154.  
DR InterPro; IPR001750; Oxidored\_q1.  
DR Pfam; PF00361; oxidored\_q1; 1.  
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.  
SQ SEQUENCE 556 AA; 62554 MW; 5613ACB0D2324BAF CRC64;

QY 13 LIRFL-----VPLGITNIAIDFGEQALN-----RGIAAYKEDAVEMLA-----SYG 53  
DB 177 LIVFLLGGLSSCFILGTSLLYNSGTTSLDGLYLINSISDVKDGADMPALTSWYKSY 236  
QY 54 LAYSIMKFTGPMSPDFKNVGLVFNKSRDRTKAVLCMVVAGAAVAFHTLIAYSDLYGI 113  
DB 237 LNFALLVFIGEL--FKVSAAPFHWSPDVYDAI-----PTIVTFVAILIAKISIFEL 288  
QY 114 INKLHVDESVSQSKTRRAFLYLAAPFFMDAMAWTHAGILLKHYSFLVGCASISDVIAQV 173  
DB 289 LELAVYHTNN-----YLSEF-----SWTVL--LLISLSFLIIGTVV---GLTQF 327  
QY 174 VFVAILLHSHLECPILLIPILSLYMGALVRCCTTCLGYKKNIHDIIPDRSGPELGGDAT 233  
DB 328 RIKRLAYSTIS-----HVGFFLLALSGC-----S 352  
QY 234 IRKMLFWMPLAILATQIRSPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGLW 293  
DB 353 IESTQAFIFVL-----IQYSISNLNV-----FIIIT---IGFSLYGYI 388  
QY 294 TEIRAVYPAFDKNNPSNKLVTSTNTVTAHHKKTFFVCMALSLTLCFVMTFNPVSEKIL 353  
DB 389 TTNKEYKDLLDKNSPIQVIS-----QLKGYFYINFLSLSLAITIF----- 430  
QY 354 IDIIG---VDPAFELCVVPLRIITFFFPVTVRAHLTG-----WMLTKKTFFVLAP- 402  
DB 431 -SFVGIPPLVGF-FAKQWLSAALDNGY-IFLTLLAILTSVIGAVVYLAIIKKIFFYLPD 487  
QY 403 -----SSVRIIVLIASVLVLPYLGHGATLGVGS 432  
DB 488 HSNIPSGIFLFKKGLIFEAGDFKGRITLISPPSITISITLIVILLIFMKNKELWSMGT 547  
QY 433 LL 434  
DB 548 IL 549

RESULT 9  
COX1\_BACSU  
ID COX1\_BACSU STANDARD; PRT; 622 AA.  
AC P24010; O34467;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cytochrome c oxidase polypeptide I (EC 1.9.3.1) (Cytochrome aa3  
DE subunit 1) (Caa-3605 subunit 1) (Oxidase aa(3) subunit 1).  
GN CTAD OR BSU14900.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=91146590; PubMed=1847686;  
RA Saraste M., Metsö T., Nakari T., Jalli T., Lauraeus M.,  
RA van der Oost J.;  
RT "The Bacillus subtilis cytochrome-c oxidase. Variations on a  
RT conserved protein theme.";  
RL Eur. J. Biochem. 195:517-525(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RA Bertero M., Presecan E., Glaser P., Richou A., Danchin A.;  
RT "Bacillus subtilis chromosomal region downstream nprA.";  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Connerston I.F., Cummings N.D., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
RA Entian K.D., Erington J., Fabret C., Ferrari E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
RA Guiseppi G., Guy B.J., Haga K., Haelegh J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
RA Parro V., Pohl T.M., Portetelle D., Porwolltik S., Prescott A.M.,  
RA Presecan E., Fujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivolta C., Ruelle E., Roche M., Rose M., Sadale Y.,  
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
RA Winters P., Wipet A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
RT subtilis";  
RL Nature 390:249-256(1997).  
CC -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY  
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-  
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE  
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN  
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2  
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3  
CC AND COPPER B. THIS CYTOCHROME C OXIDASE SHOWS PROTON PUMP ACTIVITY  
CC ACROSS THE MEMBRANE IN ADDITION TO THE ELECTRON TRANSFER.  
CC -!- CATALYTIC ACTIVITY: 4 ferredoxin + 2 H<sup>+</sup> + O<sub>2</sub> = 4 ferredoxin + 2 H<sub>2</sub>O.  
CC -!- COFACTOR: Two heme groups and copper B.  
CC -!- PATHWAY: Respiratory chain; terminal step.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 14  
CC POTENTIAL TRANSMEMBRANE DOMAINS.  
CC -!- SIMILARITY: Belongs to the heme-copper respiratory oxidase family.  
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CC -----  
DR EMBL; X54140; CAA38077.1; -;  
DR EMBL; Z98682; CAB11343.1; -;  
DR EMBL; Z99111; CAB13363.1; -;  
DR PIR; B69609; E69609.  
DR HSP; P18401; 1.FT.  
DR Subtilisin; BG10216; ctdA.  
DR InterPro; IPR000883; COX1.  
DR Pfam; PF00115; COX1; 1.  
DR PRINTS; PR01165; CYCOXIDASE1.  
DR PROSITE; PS00077; COX1; 1.  
KW Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;  
KW Hydrogen ion transport; Complete proteome.  
FT DOMAIN 1 27  
FT TRANSMEM 28 46  
FT DOMAIN 47 68  
FT TRANSMEM 69 88  
FT DOMAIN 89 110  
FT TRANSMEM 111 128  
FT TRANSMEM 128 128

FT DOMAIN 129 159  
FT TRANSMEM 178  
FT TRANSMEM 179 196  
FT TRANSMEM 197 215  
FT TRANSMEM 216 241  
FT TRANSMEM 242 261  
FT TRANSMEM 262 284  
FT TRANSMEM 285 304  
FT TRANSMEM 305 312  
FT TRANSMEM 313 331  
FT TRANSMEM 332 346  
FT TRANSMEM 347 366  
FT TRANSMEM 367 374  
FT TRANSMEM 375 391  
FT TRANSMEM 395 421  
FT TRANSMEM 422 441  
FT TRANSMEM 442 459  
FT TRANSMEM 460 479  
FT TRANSMEM 480 552  
FT TRANSMEM 553 572  
FT TRANSMEM 573 580  
FT TRANSMEM 581 604  
FT TRANSMEM 605 622  
FT TRANSMEM 73 73  
FT TRANSMEM 249 249  
FT TRANSMEM 253 253  
FT TRANSMEM 298 298  
FT TRANSMEM 299 299  
FT TRANSMEM 384 384  
FT TRANSMEM 386 386  
FT TRANSMEM 249 253  
FT TRANSMEM 120 120  
FT TRANSMEM 155 156  
FT TRANSMEM 288 288  
FT TRANSMEM 474 474  
SQ SEQUENCE 622 AA; 69107 MW; 80159F2D1D1913068 CRC64;  
Query Match 4.4%; Score 111; DB 1; Length 622;  
Best Local Similarity 19.8%; Pred. No. 0.27;  
Matches 80; Conservative 62; Mismatches 145; Indels 118; Gaps 16;  
QY 137 APPFMDAM-----ANTHAGILLKHKYS-----FLVG--CAS 165  
DB 104 SPPFNALGFWLFFFGHIFLNLFWLFGAPDAGWTSYASLSLHSGKHGIDFFVLGLQISG 163  
QY 166 ISDVIAQVFAVAILHSHLECRELLIPIL--SLYMGALV--RCTTCLGYKYNHDI 220  
DB 184 LGTLGAGINFLATININRPAQMTYRULFTWTFVVASALILFAPPELTGGLMLDLRL 223  
QY 221 --PRSGPELGCDATIRKMLSF-----WPLALILATQIRSRPVLNLFVSRDLGSSA-- 271  
DB 224 FGTNFFNPELGNTVWEHL-FWIFGHPEVYVILIPAFGIFSEVIPVFARKRLFGYSMV 282  
QY 272 -----ATEAVAILTATYPVGHMPYGMWLTETI----- 296  
DB 283 FAIVLIGLGFPMVWHMFTTGLGPIANAIFAVATMAIAIPTGKIKNWLLTIGWNVKY 342  
QY 297 -----RAVYPAFDKNNPSNKLVTSTNTVTAH-----IKKTFVCV--ALSITLCFVM 342  
DB 343 TTAMLYAVSFPSFVLGGVGTGVMALAAAADYQPHDTYFVVAHFHYVILGGVVFGLAGVH 402  
QY 343 FWTNVSEKILIDIG-VDPA-----FAELCVVPLRISFFFPVTVRAHL 387  
DB 403 FWPXPXFGKILHETMGKISFVLFITGPHLTFFIHFVGLMGMPRVVTFPLP-----GOGLE 458  
QY 388 TGLWMLTKKTFVLAPSSVLRIRIIVLGLVPLVGV---HGATL 428  
DB 459 TGNLISTIGAFMAAAVILLVNVITWSVKGEYVGADPWHGRTL 503  
RESULT 10  
PT2A\_ARATH

PT2A ARATH STANDARD; PRT; 610 AA.  
 AC P46031.  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Peptide transporter PTR2-A.  
 GN PTR2-A OR PTR2.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 FN SEQUENCE FROM N.A.  
 RC STRAIN=cv. Landsberg erecta;  
 RA MEDLINE=95003713; PubMed=7919993;  
 RX Steiner H., Song W., Naider F., Becker J.M., Stacey G.;  
 RT "An Arabidopsis peptide transporter is a member of a new class of  
 membrane transport proteins."  
 RL Plant Cell 6:1289-1299(1994).  
 CC -!- FUNCTION: Peptide transport.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the PTR2 family of transporters.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; U01171; AA53173.1; -  
 DR InterPro; IPR000109; PTR2.  
 DR Pfam; PF00854; PTR2; 1.  
 DR PROSITE; PS01022; PTR2\_1; 1.  
 DR PROSITE; PS01023; PTR2\_2; 1.  
 KW Peptide transport; Transport; Transmembrane.  
 DR TRANSMEM 71 91  
 FT TRANSMEM 131 151  
 FT TRANSMEM 161 181  
 FT TRANSMEM 187 207  
 FT TRANSMEM 247 267  
 FT TRANSMEM 273 293  
 FT TRANSMEM 300 320  
 FT TRANSMEM 400 420  
 FT TRANSMEM 430 450  
 FT TRANSMEM 475 495  
 FT TRANSMEM 511 531  
 FT TRANSMEM 541 561  
 SQ SEQUENCE 610 AA; 67518 MW; 6AE94D9E54DDA2D6 CRC64;  
 Query Match 4.3%; Score 109.5; DB 1; Length 610;  
 Best Local Similarity 18.9%; Pred No. 0.35;  
 Matches 110; Conservative 93; Mismatches 172; Indels 207; Gaps 29;  
 QY 7 LTHYPLRFLVPLGLTINIAIDFGQALNR-----GI-----AAVKE--DAV 46  
 DB 132 LSNFFTFWCYVTPVGAALIA-----DQFLGRYNTIVCSAVIVFGLITLCTAIPSVIDAG 187  
 QY 47 EMLASGLAYSLMKFTGPMDFKNGLV-----FVNSKRDRTKAVLCMVAGAI 96  
 DB 188 KSMGGFVSLIIGLTGTGK-----SNVSPUMAQLPKIPPVTKNGSKVIVDPVPT 242  
 QY 97 AAVFHTLIAYSLDGLYYIKLHVDSEVGS-----KTRAFLYLAAPFMDAMAWT 147  
 DB 243 -----TSRAYM-IFYWTIN-----VGSLSVLATTSLESTKGFVYALLPL----- 281  
 QY 148 HAGILLKHKYFLVGCASISDVIAQVFAVILLHSHLECRPELLIPILSLYMGALVRTT 207  
 DB 282 -----CVFVIPL-----ILAVSKTAPTSTLPPVPSLFV--LVKCS 317  
 QY 208 LCLGYKNTIHDIPDRSGPELGSDATIRKVLFWPLALILATQIRSPVNLVFSRDLG 267

DB 318 LLL--KTNL-----ISKLNH-----LALLLRYVKQWDLFD--ELK 354  
 QY 268 GSSAATEAVAILTATYVPVGHMPYGLMTEIRAVYPAPFDKPNFSNKIVSTNTVTAHI--- 324  
 DB 355 RALRACKIFLF---YPIVWCYQGT-----NNLSIQAGQWGTGNVSD 395  
 QY 325 --KKFTFCVMAUSLTLG-----FVMTWPNVSKILIDI-IGVDFP----- 362  
 DB 396 LQQAEDSIALIIFIPICDNIYPLLRKYNIPKPIRLITGLGFMFATSMIYAAVLQAKIY 455  
 QY 363 -----PAELCV-----VPLRTFSPPEVPTVRAHLTGMLTKTKTFVLAPSSV 405  
 DB 456 QRGPCVANFTDTCVSDISVWIIQIYAVLIAFS---EIFASITG-----LEFAFTKAPSM 508  
 QY 406 LRII-----VLIASIVLPVGLVGHGATLGVGSLLAGFVGEESTWIAIACY 450  
 DB 509 KSIITALFLFTNAFGALLSICISSTAVNPKLTMWTGTIAVTAFIAG-----IMFWVCF 561  
 QY 451 VYRKQKKKNESATGEDSNTMDPPTTEEVTDIVEMREENE 492  
 DB 562 HHYDAMEEQNLEFKRND-AUTKKDVEKVDHSMADESQ 602  
 RESULT 11  
 EXUT\_BACSU STANDARD; PRT; 422 AA.  
 AC O34456.  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hexuronate transporter.  
 GN EXUT OR BSU12360.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 FN SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RA MEDLINE=98240225; PubMed=9579062;  
 RX Rivolta C., Soldo B., Lazarevic V., Joris B., Mavel C., Karamata D.;  
 RT "A 35.7 kb DNA fragment from the Bacillus subtilis chromosome  
 containing a putative 12.3 kb operon involved in hexuronate catabolism  
 and a perfectly symmetrical hypothetical catabolite-responsive  
 element."  
 RL Microbiology 144:877-884(1998).  
 RN [2]  
 FN SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RA MEDLINE=98044033; PubMed=9384377;  
 RX Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerston I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,  
 RA Gim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,  
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mavel C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,

RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzengesser T.,  
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
RT subtilis";  
RL Nature 390:249-256 (1997).  
CC -!- FUNCTION: Aldohexuronate transport system.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the phthalate permease family.  
CC  
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CC  
CC EMBL: AF015825; AAC46332.1; -.  
CC EMBL: Z98110; CAB13093.1; -.  
CC PIR: A69853; A69853.  
CC Subtilisin; BG13210; exuT.  
DR InterPro; IPR004744; Dgal\_transporter.  
DR InterPro; IPR007114; MFS.  
DR Pfam: PF00083; sugar\_tr\_1.  
DR TIGRfam: TIGR00893; 2A0114; 1.  
DR PROSITE; PS00850; MFS; 1. Complete proteome.  
KW Transmembrane; Transport; Complete proteome.  
FT TRANSMEM 9 29 POTENTIAL.  
FT TRANSMEM 45 65 POTENTIAL.  
FT TRANSMEM 82 102 POTENTIAL.  
FT TRANSMEM 141 161 POTENTIAL.  
FT TRANSMEM 163 183 POTENTIAL.  
FT TRANSMEM 219 239 POTENTIAL.  
FT TRANSMEM 256 276 POTENTIAL.  
FT TRANSMEM 294 314 POTENTIAL.  
FT TRANSMEM 321 341 POTENTIAL.  
FT TRANSMEM 356 376 POTENTIAL.  
FT TRANSMEM 381 401 POTENTIAL.  
SQ SEQUENCE 422 AA; 45313 MW; C2E291AF347F7EDD CRC64;  
Query Match 4.2%; Score 107; DB 1; Length 422;  
Best Local Similarity 20.7%; Pred. No. 0.37;  
Matches 88; Conservative 62; Mismatches 125; Indels 150; Gaps 22;  
QY 81 RDRTKAVLCMVVAGIAAFAVHTLIAYSDGLGYIINKLHHVDESVGSKTRRAFLYLAAFPF 140  
DB 4 KKKLPVILFLAGVI-----NYLD-----RSALSIAA-PF 33  
QY 141 MD---AMAWTHAGILLKH-----KYSFLVGCASISDVIAQVVFVAILLHSHLECREPLL 191  
DB 34 IQDDLTLSATQMLGTFSSFSFGYAFNPLGGLVADRYGAKLTLFVAVV----- 81  
QY 192 IPILSLYMGALVRCCTTLCGLGYK--NTHDIIPDRSGPELGGDATIRKWLSPFWPLALILA 249  
DB 82 ---VMSLFGAV-----ALAFGVSLIILIRLPGMEGEL---SATINKVNNWEP-----P 127  
QY 250 TOR-----ISRIVNLF-VSRDLGGSSAATEAVAILTAY---PVGHMP 289  
DB 128 TORASVIGVNTSGTPLGGAISGPIVGMIAVAFSNKVSFVLMITGLIWAIVLWPKFVKEKP 187  
QY 290 YGWLTEIRAVYPADPKXNPSNKLAVSTNTVTAHKKFT-----FVCMALSLTLCFVWF 344  
DB 188 QETKEAPAIKA---ETSGKEKIPLT-----FYLKOKTVLFTAFAPFAYNYLFFFLTW 238  
QY 345 TPNVSEKILIDIIGVDFAFELCVVPLKIFSFVFFVPTVTRAHLTGWLM----- 392  
DB 239 FPS-----YLVBERG-----LSVESMSVITVIP-----WILGFIGLAAGGFVS 276  
QY 393 --TLKKTF---VLAPSSVLRIVLIVLASVLVPLGVGHGATLGVCSILLAGFVGSTWVIA 447

DB 277 DYVYKTKARKGVLFSEKRVKLVLTCLFSSAVLIGFAG-----LVATTAGAVTLVALS 326  
QY 448 ACYVYV 452  
DB 327 VFFLY 331  
RESULT 12  
LAT2 RAT  
ID LAT2 RAT STANDARD; PRT; 533 AA.  
AC Q9WVR6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Large neutral amino acids transporter small subunit 2 (L-type amino  
DE acid transporter 2).  
GN SLC7A8 OR LAT2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Small intestine;  
RX MEDLINE=99321902; PubMed=10391916;  
RA Segawa H., Fukasawa Y., Miyamoto K., Takeda E., Endou H., Kanai Y.;  
RT "Identification and functional characterization of a Na+-independent  
RT neutral amino acid transporter with broad substrate selectivity";  
RL J. Biol. Chem. 274:19745-19751 (1999).  
CC -!- FUNCTION: Sodium-independent, high-affinity transport of large  
CC neutral amino acids. Has higher affinity for L-phenylalanine than  
CC lat1. L-alanine is transported at physiological concentrations.  
CC Plays a role in basolateral (re)absorption of neutral amino acids.  
CC -!- SUBUNIT: Disulfide-linked heterodimer with the amino acid  
CC transport protein SLC3A2/4F2hc.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MANY AMINO ACID  
CC PERMEASES. GLYCOPROTEIN-ASSOCIATED AMINO ACID TRANSPORTERS (GPAT)  
CC SUBFAMILY.  
CC  
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CC  
CC EMBL: AB024400; BAA82517.1; -.  
DR InterPro; IPR002393; AA/rel\_permease1.  
DR InterPro; IPR004760; L\_AA\_transporter.  
DR InterPro; IPR004841; Permease\_region.  
DR Pfam; PF00324; aa\_permeases; 1.  
DR TIGRfam; TIGR00911; 2A0308; 1.  
KW Transport; Amino-acid transport; Transmembrane.  
FT TRANSMEM 41 61 POTENTIAL.  
FT TRANSMEM 73 93 POTENTIAL.  
FT TRANSMEM 114 124 POTENTIAL.  
FT TRANSMEM 156 176 POTENTIAL.  
FT TRANSMEM 190 210 POTENTIAL.  
FT TRANSMEM 232 252 POTENTIAL.  
FT TRANSMEM 269 289 POTENTIAL.  
FT TRANSMEM 311 331 POTENTIAL.  
FT TRANSMEM 363 383 POTENTIAL.  
FT TRANSMEM 399 409 POTENTIAL.  
FT TRANSMEM 423 443 POTENTIAL.  
FT TRANSMEM 448 468 POTENTIAL.  
SQ SEQUENCE 533 AA; 58190 MW; 99479DB60DA69DF0 CRC64;  
Query Match 4.2%; Score 107; DB 1; Length 533;  
Best Local Similarity 20.7%; Pred. No. 0.48;  
Matches 114; Conservative 78; Mismatches 192; Indels 168; Gaps 30;

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 CC -----  
 CC EMBL; U67559; AAB99180.1; -;  
 CC PIR; A64447; A64447.  
 CC TIGR; MJ1177; -;  
 CC InterPro; IPR002549; UPF0118.  
 CC Pfam; PF01594; UPF0118; 1.  
 CC Hypothetical protein; Transmembrane; Complete proteome.  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 13 33 POTENTIAL.  
 FT TRANSMEM 61 81 POTENTIAL.  
 FT TRANSMEM 138 158 POTENTIAL.  
 FT TRANSMEM 191 211 POTENTIAL.  
 FT TRANSMEM 234 254 POTENTIAL.  
 FT TRANSMEM 259 279 POTENTIAL.  
 FT TRANSMEM 293 313 POTENTIAL.  
 SQ SEQUENCE 334 AA; 38445 MW; FD7429A229130200 CRC64;  
 CC -----  
 CC Query Match 4.2%; Score 106; DB 1; Length 334;  
 CC Best Local Similarity 19.3%; Pred. No. 0.34;  
 CC Matches 74; Conservative 71; Mismatches 111; Indels 128; Gaps 19;  
 CC -----  
 QY 133 LYLAAPEPDMAWTHAGI-----LLKHYSFLVGCA-SIS-----DVLQV 174  
 Db 22 LYI-WPFDVLAYSCAPAYMALPVNIRKFNKTISAGLAISIVLPMITITVALLT 80  
 QY 175 FVAILHSHLECEPRLIPILSY-----MGALVRCCTCLGYYKN-IHDIIDRSQPELG 229  
 Db 81 FMEIILSFNTKSTIEPVINEILSYNSFMLEIRINEQIIAKYIDEFIKLVQFSKIID 140  
 QY 230 GDATIRKMSFWWPLALILATQIRISPIVNLVSRDLGGSSAATEAVAILTATYPVGHMP 289  
 Db 141 VGVLIVKVI-----WVL-----FTTFPLRD--GDKXNLIISFPDEY----- 177  
 QY 290 YGWLTEIRAVYPAPDKNPNKLVSTNTVTAHKKFTFVCMALSLTLCFVNFVTPNVS 349  
 Db 178 ---KXKRIYLSYLDHSDYKNLFS-----LGMMVYISIAIYFFLIHDTKA 211  
 QY 350 EKILIDIIIGVDFAFELCVVPLRIFSPFPVPTVRAHLTGMLTL-----KK 396  
 Db 212 --IGYLILGV--PYAEFLAITGIFALLPI-----LGMMVYISIAIYFFLIHDTKA 260  
 QY 397 TFV-----LAPSSVLR-----IIVLIASLVLPYLVGHGATLVGSLLA 435  
 Db 261 VFMFIYGEFLSLAPDFVIRPVLVKEVDHPVLVVIAPLWAPLSLGLSG--PAIGFLV 318  
 QY 436 GFVGESTWVAIAACVYRKQKKM 459  
 Db 319 G-----ALNAPYLAKYRDKKI 334  
 CC -----  
 CC RESULT 14  
 CC LSGI\_HABIN STANDARD; PRT; 401 AA.  
 ID LSGI\_HABIN STANDARD; PRT; 401 AA.  
 AC P71399; Q48210;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lsg locus putative protein 1.  
 GN H1700.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OC NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A2;  
 RA McLaughlin R., Abu Kwaik Y., Young R., Spinola S., Apicella M.;

QY 37 GIAAVKEDAVEMLASYGILAYSLM---KEFTGMSDFKVGVLVFNYSKDRTKAVLQMWVA 93  
 Db 34 GVALKKE--IGLSACGIIVNGIISGIFVSPKGVLENAGSVGL-----ALIVMIT 83  
 QY 94 GAIAAVFHTLAYSGLGYIINKLHVHDESIG--SKTRRAFLYLAAFPFMDAMAWTHAGI 151  
 Db 84 GVITAV--GALCYAELGVTI-----PKSGDISYVKDIFGGLAGP-----LRLW--IAV 128  
 QY 152 LLKHYSFLVGCAISDSDVIAQVVF-----VAILHSHLECRE----- 188  
 Db 129 LIVIPTNQAVIALTFNSVVLQPLPTCPPEPSGLRLAAICLLLTWNVCSSVRWATRVQ 188  
 QY 189 -----PLLIIPILSYMGALVRCCTCLGYY-----KNIHDIIDRSQPELGSDATIRKM 237  
 Db 189 DIFTAGKLALALIIINGW---QICKGEFFWLEPRNAFENFOR---PDIGLVALAFLQ 241  
 QY 238 LSF---WWPLALILATORISRPVNL-----FVSRDLGGSSA-----AT 273  
 Db 242 GSFAVGGWNP-LNYVTEELVDPYKNLPRAIFISPLVTFVVFANIAVVTAMSPQELLAS 300  
 QY 274 EAVAILTATYPVGHMPYQWLTEIRAVYPAPDKNPNKLVST-----NTVT 320  
 Db 301 NAVAVTFGEKLLGVN--AWIMPIVSALSTFGGVNGS--LFTSSRLFFAGAREGHLPSVLA 356  
 QY 321 AAHIKKFT-----FVCMALSLTLCFVNFVTPNVSSEKILIDIIG-VDPAPAEELCVV--- 369  
 Db 357 MHVRCRTPIPALLFTCLSLTLMVTSDMYT-----LINVGFINVLFYGVTVAGQIV 409  
 QY 370 -----PLRISFPFPVPTVRAHLTGMLTKTFVLAPSLSVLRIVLIASLVLP 419  
 Db 410 LRWKKPDPRIPIKISLLFPI-----IYLLFWAFL--IFSLWSEFPVVGIGLAIMLTGVP 462  
 QY 420 --YLVGHGATLVGSLAGFVGESTWVAIAACVYRKQKKVNESEAFEGEDSAMTDMPP 477  
 Db 463 VVFLGYVQW--HKPKCFNDFIESLTIVSQKCVVYVQ-----EGDSGT----- 505  
 QY 478 TBEVTDIVEMRE 489  
 Db 506 -ETIDVEEQHK 516  
 CC -----  
 CC RESULT 13  
 CC YB77\_METJA STANDARD; PRT; 334 AA.  
 ID YB77\_METJA STANDARD; PRT; 334 AA.  
 AC Q58578;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein MJ1177.  
 GN MJ1177.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
 OC Methanocaldococcaceae; Methanocaldococcus.  
 OC NCBI\_TaxID=2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RA MEDLINE=96337999; PubMed=8688087;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,  
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 Science 273:1058-1073 (1996).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY.  
 CC -----

"Characterization and sequence of the *lsq* locus from *Haemophilus influenzae*,"  
Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.

```

[2]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=9535630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierulff A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudke D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrman J.J., Geoghagan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."
RL Science 269:496-512(1995).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: Belongs to the polysaccharide synthase family.
CC HI0867/H11700 SUBFAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
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DR EMBL; M94855; AAC24978.1; -;
DR EMBL; U32842; AAC23346.1; ALT_INIT.
DR PIR; H64175; H64175.
DR TIGR; H11700; -;
DR InterPro; IPR002797; Polysacc_synt.
DR Pfam; EF01943; Polysacc_synt; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 36 56 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 132 152 POTENTIAL.
FT TRANSMEM 162 182 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
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FT TRANSMEM 282 302 POTENTIAL.
FT TRANSMEM 320 340 POTENTIAL.
FT TRANSMEM 352 372 POTENTIAL.
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FT TRANSMEM 249 249 V -> I (IN REF. 1).
FT CONFLICT 276 276 V -> I (IN REF. 1).
FT CONFLICT 358 358 I -> V (IN REF. 1).
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SQ SEQUENCE 401 AA; 45944 MW; FE2E7B02747B0874 CRC64;
Query Match 4.2%; Score 105; DB 1; Length 401;
Best Local Similarity 18.8%; Pred. No. 0.5;
Matches 75; Conservative 62; Mismatches 133; Indels 128; Gaps 17;
QY 106 YSDLOYIYINKLHVDSVGSKTRAFIYLAAPFMDAMWTHAGILKHKYSP----- 159
Db EMBL; U32842; AAC23346.1; ALT_INIT.
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QY 190 -LLIFILSLYGVALVRCITCLGYKYNTHDIIPDRSGPELGDATI-----RK----- 236
Db YAFIQFSLTVTGAVF--VALLLEYQN--DLVEKRILAILLSNLVWVFFSYFLYRKSTTS 189
QY 237 -----MLSEWFWPLALILATORISRPVNLV-----SRDLGSSAAATEAVA 277
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QY 397 TFLVAPSSVLRIRIIVLIASLVL-----PYLGVHGA 426
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RESULT 15
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AC Q8TJA9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pyrophosphate-energized proton pump 1 (EC 3.6.1.1) (Pyrophosphate-
DE energized inorganic pyrophosphatase 1) (H+-Ppase 1) (Membrane-bound
DE proton-translocating pyrophosphatase 1).
GN HPPA1 OR MA3879.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
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RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Ye W., A.M.,
RA Hedderich R., Ingram-Smith C., Kuettnar H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
CC -|- FUNCTION: Generates a proton motive force; it probably catalyzes a
CC fully reversible reaction, thus being able to synthesize
CC pyrophosphate when the proton motive force is sufficient (By
CC similarity).
CC -|- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -|- COFACTOR: Magnesium and potassium (By similarity).
CC -|- SUBUNIT: Homodimer (potential).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -|- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase
CC (TC 3.A.10) family. Subfamily 1.
CC
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CC
CC -----
DR EMBL; AS011099; AM07230.1; ALT_INIT.
DR HAMAP; MF_01129; -; 1.
DR InterPro; IPR004131; H_Ppase.
DR Pfam; PF03030; H_Ppase; 1.
DR TIGRfams; TIGR01104; V_Ppase; 1.
KW Hydrogen ion transport; Hydrolase; Magnesium; Potassium;
KW Transmembrane; Complete proteome.
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Query Match 4.2%; Score 105; DB 1; Length 676;
Best Local Similarity 21.0%; Pred. No. 0.91;
Matches 88; Conservative 50; Mismatches 145; Indels 136; Gaps 17;

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Db 281 VGTFFVTRNTKTESAIHMAFNGLIAAILTVIA---SYFVTS----- 320

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Search completed: April 22, 2004, 13:56:56  
Job time : 21 secs



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3	1264	42.9	1383	29	AY417273		Homo sapi
4	1049.6	35.6	1383	29	AY417275		Mus muscu

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grinwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalhus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 2980)  
Direct Submission  
Strausberg, R.  
Submitted (02-JAN-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [ang@bcm.tmc.edu](mailto:ang@bcm.tmc.edu)  
Gunararatne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounsgood, H.,  
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 61 Row: c Column: 11  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994166  
This clone has the following problem: frame shifted.

Location/Qualifiers

## source

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/strain="FVB/N"
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ductal Carcinoma, 5 month old virgin mouse."
/clone_lib="NCI CGAP_Mam6"
/lab_host="DH10B"
/notes="pCMV-SPORT6"

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## ORIGIN

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QY	73	GGCGGGACATAGGTGAAATTCGCGGGCTCAACGCACTACTGCGCCCTGATCCGGTTCCT	132	
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VERSION AK083135.1  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
2  
REFERENCE  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Komori, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
3  
REFERENCE  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
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Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
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DEFINITION Homo sapiens ANKH gene, VIRUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417273  
VERSION AY417273.1 GI:39773233  
KEYWORDS GSS.

AY417273 1383 bp DNA linear GSS 17-DEC-2003  
Homo sapiens ANKH gene, VIRUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
AY417273  
AY417273.1 GI:39773233  
GSS.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1383)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1383)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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RESULT 4  
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DEFINITION Mus musculus ANKH gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417275  
VERSION AY417275.1 GI:39773235  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1383)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1383)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source Location/Qualifiers  
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/organism="Mus musculus"  
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Query Match 35.6%; Score 1049.6; DB 29; Length 1383;  
Best Local Similarity 81.7%; Pred. No. 4.8e-209;  
Matches 1130; Conservative 0; Mismatches 253; Indels 0; Gaps 0;  
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QY 359 GCAGGGGCCATCGCTCCGCTCTTTCACACATGATGATCTTATAGTGATTAGGACTACTAC 418  
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LOCUS Pan troglodytes ANKH gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY417274  
VERSION AY417274.1 GI:39773234  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
REFERENCE 1 (bases 1 to 1047)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,



Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 1047)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
 Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B.,  
 Ferris, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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RESULT 6  
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 VERSION BX385283.1 GI:30447347  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1059)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 3147.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DL009AB03QPI&cluster=3147.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Paraday Avenue Genoscope sequence ID : CS0DL009AB03QPI.

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 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN









Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 The following repetitive elements were found in this cDNA  
 sequence: 95-123, >AT-rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

source

Location/Qualifiers  
 1. 771  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-E10-ayd-b-01-0-UI"  
 /tissue\_type="Chondrosarcoma"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP E10"  
 /note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)  
 with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 NCI CGAP E10 is a cDNA library containing the following  
 tissue(s): Chondrosarcoma. The library was constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into p773-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is ACACCTTGAC.  
 TAG TISSUE=chondrosarcoma  
 TAG\_LIB=UI-H-E10  
 TAG\_SEQ=ACACCTTGAC"

## ORIGIN

Query Match 25.0%; Score 737; DB 14; Length 771;  
 Best Local Similarity 99.7%; Pred. No. 1.4e-143;  
 Matches 748; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2196 ATCTCCCGTAGAAGGTTGGTTTGAATGCCCCGGGGCGACCACTGACATGGTTGAA 2255  
 DB 759 ATCTCCCGTAGAAGGTTT-GTNTGAATGCCCGGGGCGACCACTGACATGGTTGAA 701  
 QY 2256 TGATAGCATTTTCACCTCTGGTCTCTAGATCTGAGCAAGCTGTCTGAGTTCTCACCCCCAC 2315  
 DB 700 TGATAGCATTTTCACCTCTGGTCTCTAGATCTGAGCAAGCTGTCTGAGTTCTCACCCCCAC 641  
 QY 2316 CGTGTATATACATGAGCTAACTTTTAAATGTGCACAAAGCGCATCTCCAGATTCGAG 2375  
 DB 640 CGTGTATATACATGAGCTAACTTTTAAATGTGCACAAAGCGCATCTCCAGATTCGAG 581  
 QY 2376 ACCCTGCCGATGACTTTTCCGAGGCTTGCTTTTCCCTGCTCCCTTCTCTGAAGTGGCA 2435  
 DB 580 ACCCTGCCGATGACTTTTCCGAGGCTTGCTTTTCCCTGCTCCCTTCTCTGAAGTGGCA 521  
 QY 2436 TTAGACGAGTCACATGGAGCATCTTAATTTGCAATTTAGTTTTCACAGTGAATGAAG 2495  
 DB 520 TTAGACGAGTCACATGGAGCATCTTAATTTGCAATTTAGTTTTCACAGTGAATGAAG 461  
 QY 2496 CTTTAAGTCTCATCCAGCATCTTAATCCAGGCTGCTGTAGGTAACCTTTTGAAGTAGAT 2555  
 DB 460 CTTTAAGTCTCATCCAGCATCTTAATCCAGGCTGCTGTAGGTAACCTTTTGAAGTAGAT 401  
 QY 2556 ATATTACCTGGTTCTCTATCTCTAGTCATAACTCTGCGGTACAGGTAATTTGAGATGTA 2615  
 DB 400 ATATTACCTGGTTCTCTATCTCTAGTCATAACTCTGCGGTACAGGTAATTTGAGATGTA 341  
 QY 2615 CTACGGTACTTCCCTCCGACACATACGATAGAGACATTTTATACGATACACAG 2675

DB 340 CTACGGTACTTCCCTCCACACCATACGATAAGCAAGACATTTTATACGATACACAG 281  
 QY 2676 TCACATATGTGTCCTCCCTCGAAATACCATTCGAAATCCATGCGATGCGATATATTTT 2735  
 DB 280 TCACATATGTGTCCTCCCTCGAAATACCATTCGAAATCCATGCGATGCGATATATTTT 221  
 QY 2736 CTAAGTTTGGAAACGAGGTTTTTCTTTTAAATAAATATAGACACGGTTTCACTAAATT 2795  
 DB 220 CTAAGTTTGGAAACGAGGTTTTTCTTTTAAATAAATATAGACACGGTTTCACTAAATT 161  
 QY 2796 GATTTAGTCAGAAATCTTAGACTGAAAGACCTAAACAAAAAATATTTTAAAGATATAA 2855  
 DB 160 GATTTAGTCAGAAATCTTAGACTGAAAGACCTAAACAAAAAATATTTTAAAGATATAA 101  
 QY 2856 ATATATGCTGTATATGTTATGTAATTTATTTAGCTATATATACATTTTCCATTTTCGCA 2915  
 DB 100 ATATATGCTGTATATGTTATGTAATTTATTTAGCTATATATACATTTTCCATTTTCGCA 41  
 QY 2916 TTTTCAATAAATGCTCTTAATACAAAAA 2945  
 DB 40 TTTTCAATAAATGCTCTTAATACAAAAA 11

## RESULT 10

BE793798

LOCUS

DEFINITION

mRNA sequence.

ACCESSION

BE793798

VERSION

BE793798.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 760)

AUTHORS

NIH-MGC

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: LLC800 row: m column: 14  
 High quality sequence stop: 719.

FEATURES

Location/Qualifiers

1. 760

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3944245"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_7"

/notes="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 25.0%; Score 735.2; DB 10; Length 760;  
 Best Local Similarity 98.8%; Pred. No. 3.4e-143;  
 Matches 751; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

125 CGGTTCTTGGTGGCCCTGGGCGATCACCACATAGCCATCGATCTCGGGAGCAGCCCTTG 184  
Db 1 CGGTTCTTGGTGGCCCTGGGCGATCACCACATAGCCATCGATCTCGGGAGCAGCCCTTG 60  
Qy 185 AACCGGGGATTCGCTGCTGCAAGGAGGATGAGTGGATGCTGCGGAGTACCGGCTG 244  
Db 61 AACCGGGGATTCGCTGCTGCAAGGAGGATGAGTGGATGCTGCGGAGTACCGGCTG 120  
Qy 245 GGGTACTCCTCATGAAGTCTTTCACGCTGCCATGAGTCTTCAAAATGTTGGCCCTG 304  
Db 121 GGGTACTCCTCATGAAGTCTTTCACGCTGCCATGAGTCTTCAAAATGTTGGCCCTG 180  
Qy 305 GTGTTTGTGAACAGCAGAGAGACAGGACCAAGGCTGCTGATGTTGGTGGTGGCAGG 364  
Db 181 GTGTTTGTGAACAGCAGAGAGACAGGACCAAGGCTGCTGATGTTGGTGGTGGCAGG 240  
Qy 365 GCATCGCTCCGCTCTTTCACACACTGATGATCTTATGATTTAGGATPACTACATTATC 424  
Db 241 GCATCGCTCCGCTCTTTCACACACTGATGATCTTATGATTTAGGATPACTACATTATC 300  
Qy 425 AATAAATTCACATGTCGAGGAGTGGTGGGAGCAGACAGAGAGGCGCTTCTGTAC 484  
Db 301 AATAAATTCACATGTCGAGGAGTGGTGGGAGCAGACAGAGAGGCGCTTCTGTAC 360  
Qy 485 CTCGCCGCTCTTTCATGACGCAATGGCATGGACCCATGCTGGCATCTCTTAAAA 544  
Db 361 CTCGCCGCTCTTTCATGACGCAATGGCATGGACCCATGCTGGCATCTCTTAAAA 420  
Qy 545 CACAAATACAGTTCTGCTGGGATGCTGCTCAATCTGAGTGTATGATGCTGAGTTGTT 604  
Db 421 CACAAATACAGTTCTGCTGGGATGCTGCTCAATCTGAGTGTATGATGCTGAGTTGTT 480  
Qy 605 TTGTAGCCATTTTGTCTTACAGTACCTGGAATGCGGGAGCGCTGCTATCCCGATC 664  
Db 481 TTGTAGCCATTTTGTCTTACAGTACCTGGAATGCGGGAGCGCTGCTATCCCGATC 540  
Qy 665 CTCCTCTTGTATAGGCGCATTTGTCGCTGCAACACCTGTCGCTGGCTTACTACAAG 724  
Db 541 CTCCTCTTGTATAGGCGCATTTGTCGCTGCAACACCTGTCGCTGGCTTACTACAAG 600  
Qy 725 AACATTACAGATCATCTCCACAGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCAATA 784  
Db 601 AACATTACAGATCATCTCCACAGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCAATA 660  
Qy 785 AGAAGATGCTGAGCTTCTGTTGGCTTTGGCTCTAATTTCTGGCCACACAGAGATCAGT 844  
Db 661 AGAAGATGCTGAGCTTCTGTTGGCTTTGGCTCTAATTTCTGG-CACACAGAGATCAGT 719  
Qy 845 CGGCCTATTGTCAACCTCTTTGTTCCCGGACCTTGGTG 884  
Db 720 CGTGCTATTGTCAACTCTTTGTTTCCCGGACCTTGGTG 759

RESULT 11  
BU615215  
LOCUS  
DEFINITION BU615215 737 bp mRNA linear EST 23-SEP-2002  
UI-H-FHO-bcg-m-04-0-UI.s1 NCI\_CGAP\_FHO Homo sapiens cDNA clone  
UI-H-FHO-bcg-m-04-0-UI 3', mRNA sequence.  
ACCESSION BU615215  
VERSION 1 (bases 1 to 737)  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 737)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: James Martin

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Seq primer: M13 FORWARD  
POLYA=No.

FEATURES  
source  
1. 737  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FHO-bcg-m-04-0-UI"  
/tissue\_type="Human Chondrosarcoma Cell Line"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_l1b="NCI\_CGAP\_FHO"  
/notes="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI\_CGAP\_FHO is a cDNA library containing the following  
tissue(s): Human Grade I Chondrosarcoma Cell Line The  
library was constructed according to Bonaldo, Lennon and  
Soares, Genome Research, 6:791-806, 1996. First strand  
cDNA synthesis was primed with an oligo-dT primer  
containing a Not I site. Double stranded cDNA was ligated  
to an EcoR I adaptor, digested with Not I, and cloned  
directionally into pT73-Pac vector. The oligonucleotide  
used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dT)18 tail. The sequence tag for this  
library is AGAATCCGCG. The cell line was provided by Dr  
James Martin from University of Iowa  
TAG TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1  
Chondrosarcoma  
TAG\_LAB=UI-H-FHO  
TAG\_SEQ=AGAATCCGCGC"

ORIGIN  
Query Match 24.5%; Score 720.4; DB 13; Length 737;  
Best Local Similarity 99.5%; Pred. No. 4.3e-140;  
Matches 732; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1655 TTTTGTCTTCTTTGGTAATGAAGAGGCTTGAATTAAGGTTTCGTCAATCTCTA 1714  
Db 2 TTTTGTCTTCTTTGGTAATGAAGAGGCTTGAATTAAGGTTTCGTCAATCTCTA 61  
Qy 1715 GCATCTGGGTATGCTCACACTGACGCGGGGACCTAGTGAATGCTTTTACTTGTCTAT 1774  
Db 62 GCATCTGGGTATGCTCACACTGACGCGGGGACCTAGTGAATGCTTTTACTTGTCTAT 121  
Qy 1775 GTAAAAACAAACGAAACAACTGACTTCATACCCCTGCTCACGAAACCCAAAGACACA 1834  
Db 122 GTAAAAACAAACGAAACAACTGACTTCATACCCCTGCTCACGAAACCCAAAGACACA 181  
Qy 1835 GCTGCCTCAGGTTGAGTTGCTCTCTCCCTCGGACATCTCTCTTGGACCAAG 1894  
Db 182 GCTGCCTCAGGTTGAGTTGCTCTCTCCCTCGGACATCTCTCTTGGACCAAG 241  
Qy 1895 GATGACAGTGTGCGCATCGCGCTCGGTTCACCTGACAGCAGGCCACAGACTCTCTGT 1954  
Db 242 GATGACAGTGTGCGCATCGCGCTCGGTTCACCTGACAGCAGGCCACAGACTCTCTGT 301  
Qy 1955 CCGCTTTCATCGCTCTTAAGATCAACAGTTAAACTGGCTTCTTTGATTGCTTCC 2014  
Db 302 CCGCTTTCATCGCTCTTAAGATCAACAGTTAAACTGGCTTCTTTGATTGCTTCC 361  
Qy 2015 CAGTCATCGGCGTACAAAGAGATGAGCCCGGTGGCTCTTAAATTTCCCTTCTGCC 2074  
Db 362 CAGTCATCGGCGTACAAAGAGATGAGCCCGGTGGCTCTTAAATTTCCCTTCTGCC 421  
Qy 2075 ACGGAGTTCGAAACCATCTACTCCACATGACAGAGGCGGGTGGACGTCAGCCCGG 2134  
Db 422 ACGGAGTTCGAAACCATCTACTCCACATGACAGAGGCGGGTGGACGTCAGCCCGG 481

QY 2135 AGTCCCGGTTACACTGAGGAACGAGACCTGTGACACACAGCAGGCTGACAGATGACAG 2194  
Db 482 AGTCCCGGTTACACTGAGGAACGAGACCTGTGACACACAGCAGGCTGACAGATGACAG 541  
QY 2195 AATCTCCCGTAGAAGGTTGGTTTGAATGCCCGGGGCGAGCAAACTGACATGGTTGA 2254  
Db 542 AATCTCCCGTAGAAGGTTGGTTTGAATGCCCGGGGCGAGCAAACTGACATGGTTGA 601  
QY 2255 ATGATAGCAATTTCACTCTGGTCTCTCTAGATCTGACAGCTGCTGAGTTCTCACCCCA 2314  
Db 602 ATGATAGCAATTTCACTCTGGTCTCTCTAGATCTGACAGCTGCTGAGTTCTCACCCCA 661  
QY 2315 CCGT-GTATATACATGAGCTAACTTTTAAATGTTCACAAAAGCGCATCTCCAGATTCC 2373  
Db 662 CCGTGTATATACATGAGCTAACTTTTAAATGTTCACAAAAGCGCATCTCCAGATTCC 721  
QY 2374 AGACCTGCCGATGA 2389  
Db 722 AGACCTGCCGATGA 737

RESULT 12  
LOCUS BE876197 723 bp mRNA linear EST 20-OCT-2000  
DEFINITION 601486717F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3889037 5',  
mRNA sequence.

ACCESSION BE876197  
VERSION BE876197.1 GI:10325077  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: DCTD/DRP/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLN9670 row: a column: 06  
High quality sequence stop: 719.  
Location/Qualifiers  
1..723

FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3889037"  
/tissue\_type="large cell carcinoma, undifferentiated"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_69"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."

ORIGIN  
Query Match 24.4%; Score 718.8; DB 10; Length 723;  
Best Local Similarity 99.7%; Pred. No. 9.2e-140;  
Matches 720; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 914 ATTGTGAGGCACATACCTGTGGTGCATGCGATGCGTGGTTGACGGAATCCGT 973  
Db 1 ATTGTGAGGCACATACCTGTGGTGCATGCGATGCGTGGTTGACGGAATCCGT 60

QY 974 GCTGTGTATCTCTGCTTCGCAAGAATAACCCGACCAAACTCGTGAGCAGCAAC 1033

Db 61 GCTGTGTATCTCTGCTTCGCAAGAATAACCCGACCAAACTCGTGAGCAGCAAC 120  
QY 1034 ACAGTCAGCGGAGCCACATCAAGAAGTTCACTTCGTCGATGGCTCTGTCTACTCAG 1093  
Db 121 ACAGTCAGCGGAGCCACATCAAGAAGTTCACTTCGTCGATGGCTCTGTCTACTCAG 180  
QY 1094 CTCTCTTTCTGATGATTTTGGACACCCAACTGCTGAGAAAACTTTGATAGACATCATC 1153  
Db 181 CTCTCTTTCTGATGATTTTGGACACCCAACTGCTGAGAAAACTTTGATAGACATCATC 240  
QY 1154 GGAGTGGACTTTTCCCTTTGGAGAACTCTGTGTTGTTCCCTTGGCGATCTTCTCTCTTC 1213  
Db 241 GGAGTGGACTTTTCCCTTTGGAGAACTCTGTGTTGTTCCCTTGGCGATCTTCTCTCTTC 300  
QY 1214 CCAGTTCCAGTTCACAGTGGGCGCATCTCACCCGGTGGCTGATGACACACTGAAGAAACC 1273  
Db 301 CCAGTTCCAGTTCACAGTGGGCGCATCTCACCCGGTGGCTGATGACACACTGAAGAAACC 360  
QY 1274 TTCTGCTTTGCCCCAGCTCTGTGCTGCGATCATCTGTCCTCATCGCCAGCTCTGTGCTC 1333  
Db 361 TTCTGCTTTGCCCCAGCTCTGTGCTGCGATCATCTGTCCTCATCGCCAGCTCTGTGCTC 420  
QY 1334 CTACCTCTACCTGGGGGTCAGCGTGGCGCTGGGCTGGGCTCCCTCTCTCGGGGCTTT 1393  
Db 421 CTACCTCTACCTGGGGGTCAGCGTGGCGCTGGGCTGGGCTCCCTCTCTCGGGGCTTT 480  
QY 1394 GTGGGAGAAATCCATGCTGCCATCGCTGCTGTATGCTTACCGGAAACGAGAAAG 1453  
Db 481 GTGGGAGAAATCCATGCTGCCATCGCTGCTGTATGCTTACCGGAAACGAGAAAG 540  
QY 1454 AAGATGGAGAAATGAGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1513  
Db 541 AAGATGGAGAAATGAGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
QY 1514 ACAGAGGAGGTGACAGACATCGTGAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1573  
Db 601 ACAGAGGAGGTGACAGACATCGTGAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
QY 1574 CATGGGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1633  
Db 661 CATGGGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
QY 1634 CA 1635  
Db 721 CA 722

RESULT 13  
LOCUS BQ014252/c  
DEFINITION UI-H-ED1-axs-d-21-0-UI-s1 NCI CGAP ED1 Homo sapiens cDNA clone  
IMAGE:3832932 3', mRNA sequence.

ACCESSION BQ014252  
VERSION BQ014252  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 732)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

JOURNAL CONTACT: Robert Strausberg, Ph.D.  
COMMENT Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Jose Mercuende  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

The following repetitive elements were found in this cDNA  
sequence: 95-123, >AT rich#Low\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
1..732  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5832932"  
/tissue\_type="Chondrosarcoma"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP ED1"  
/note="Organ: Left Pubic Bone; Vector: p7T3-Pac  
(Pharmacia) with a modified polylinker; Site 1: EcoR I;  
Site 2: Not I; NCI CGAP ED1 is a normalized cDNA library  
containing the following tissue(s): Chondrosarcoma cell  
line C55. The library was constructed according to  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into p7T3-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is GCTCAAGGCT.  
TAG\_TISSUE=chondrosarcoma  
TAG\_LIB=UI-H-ED1  
TAG\_SEQ=CGTCAAGGCT"

ORIGIN

Query Match 24.4%; Score 717.4; DB 12; Length 732;  
Best Local Similarity 99.9%; Pred. No. 1.8e-139; Indels 0; Gaps 0;  
Matches 718; Conservative 0; Mismatches 13

QY 2227 CCGCGGGGAGCAAACTGACATGTTGAATGATAGCATTTCACTGCGTTCTCTAGAT 2286  
DB 729 CCGCGGGGAGCAAACTGACATGTTGAATGATAGCATTTCACTGCGTTCTCTAGAT 670  
QY 2287 CTGAGCAAGCTGTCAGTTCTCACCCCGGCGGTATATACATGAGTAACTTTTAAAT 2346  
DB 669 CTGAGCAAGCTGTCAGTTCTCACCCCGGCGGTATATACATGAGTAACTTTTAAAT 610  
QY 2347 TGTCACAAAAGCGCATCTCCAGATTCAGACCCCTGCGGATGACTTTTCTGAAGGCTTG 2406  
DB 609 TGTCACAAAAGCGCATCTCCAGATTCAGACCCCTGCGGATGACTTTTCTGAAGGCTTG 550  
QY 2407 CTTTTCCTCGCTTCTTCTGAAGTTCGATAGAGCGAGTCACATGAGCATCTTAACCT 2466  
DB 549 CTTTTCCTCGCTTCTTCTGAAGTTCGATAGAGCGAGTCACATGAGCATCTTAACCT 490  
QY 2467 TGCATTTTGTGTTTTCAGTGAAGTCTTGAAGTCTCATCCAGCATCTTAATGCCAG 2526  
DB 489 TGCATTTTGTGTTTTCAGTGAAGTCTTGAAGTCTCATCCAGCATCTTAATGCCAG 430  
QY 2527 GTTCTGTAGGTAACCTTTTGAAGTAGATATATPACCTGTTCTGCTATCCTTAGTCATA 2586  
DB 429 GTTCTGTAGGTAACCTTTTGAAGTAGATATATPACCTGTTCTGCTATCCTTAGTCATA 370  
QY 2587 ACTTCGGGTACAGTAATGAGATGCTACGCTACTTCCCTCCACACCATACGATA 2646  
DB 369 ACTTCGGGTACAGTAATGAGATGCTACGCTACTTCCCTCCACACCATACGATA 310  
QY 2647 AAGCAAGACATTTTATACGATACAGAGTCACATATGTGTCTCTCCCTGAAATAAGCAT 2706  
DB 309 AAGCAAGACATTTTATACGATACAGAGTCACATATGTGTCTCTCCCTGAAATAAGCAT 250  
QY 2707 TCGAAATCCATGCGAGTATATTTTCTAAGTTTGGAAAGCAGGTTTTTCCCTTA 2766  
DB 249 TCGAAATCCATGCGAGTATATTTTCTAAGTTTGGAAAGCAGGTTTTTCCCTTA 190

QY 2767 AAAAAATTATACACACGGTTCTACTAAATTTGATTTAGTTCAGATTTCTAGACTGAAGAAC 2826  
DB 189 AAAAAATTATACACACGGTTCTACTAAATTTGATTTAGTTCAGATTTCTAGACTGAAGAAC 130  
QY 2827 CTAACCAAAAAAATATTTTAAAGATATATAATATATGCTGTATATGTTATGTTATTT 2886  
DB 129 CTAACCAAAAAAATATTTTAAAGATATATAATATATGCTGTATATGTTATGTTATTT 70  
QY 2887 TAGGCTATATACATTTCTCTATTTTCGCATTTTCAATAAAATGCTCTTAATAACAAAA 2945  
DB 69 TAGGCTATATACATTTCTCTATTTTCGCATTTTCAATAAAATGCTCTTAATAACAAAA 11

RESULT 14  
BQ009716/c

LOCUS BQ009716 729 bp mRNA linear EST 26-MAR-2002  
DEFINITION UI-H-ED0-aya-d-17-0-UI.s1 NCI CGAP\_ED0 Homo sapiens cDNA clone  
IMAGE:5836000 3', mRNA sequence.

ACCESSION BQ009716

VERSION BQ009716.1 GI:19734617

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 729)

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TUMOR GENE INDEX

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

The following repetitive elements were found in this cDNA

sequence: 95-123, >AT rich#Low\_complexity (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
1..729

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5836000"

/tissue\_type="Chondrosarcoma"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP ED0"

/note="Organ: Left Pubic Bone; Vector: p7T3-Pac

(Pharmacia) with a modified polylinker; Site 1: EcoR I;

Site 2: Not I; NCI CGAP\_ED0 is a cDNA library containing

the following tissue(s): Chondrosarcoma cell line C55. The

library was constructed according to Bonaldi, Lennon and

Soares, Genome Research, 6:791-806, 1996. First strand

cDNA synthesis was primed with an oligo-dT primer

containing a Not I site. Double stranded cDNA was ligated

to an EcoR I adaptor, digested with Not I, and cloned

directionally into p7T3-Pac vector. The oligonucleotide

used to prime the synthesis of first-strand cDNA contains

a library tag sequence that is located between the Not I

site and the (dT)18 tail. The sequence tag for this

library is GCTCAAGGCT

TAG\_TISSUE=chondrosarcoma

TAG\_LIB=UI-H-ED0

TAG\_SEQ=CGTCAAGGCT"

ORIGIN

Query Match 24.3%; Score 717; DB 12; Length 729;

Best Local Similarity 99.7%; Pred. No. 2.2e-139;



Matches 717; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2227 CC0GGGGGCGAAGTACATGCTTGAATGATAGCATTTCACTGCGCTTCTCTAGAT 2286

Db 729 CC0GGGGGCGAAGTACATGCTTGAATGATAGCATTTCACTGCGCTTCTCTAGAT 670

QY 2287 CTGAGCAAGCTGTGCTGCTTCTCACCCCGGCTGTATATACATGAGCTAACTTTTAAAT 2346

Db 669 CTGAGCAAGCTGTGCTGCTTCTCACCCCGGCTGTATATACATGAGCTAACTTTTAAAT 610

QY 2347 TGTCAAAAAGCGATCTCCGATTCAGACCCCTGCGGATGACTTTTCTGAGGCTTG 2406

Db 609 TGTCAAAAAGCGATCTCCGATTCAGACCCCTGCGGATGACTTTTCTGAGGCTTG 550

QY 2407 CTTTTCCCTCCCTTCTGAGGTGCAATGAGCGAGTCAATGAGCATCTCTAACTT 2466

Db 549 CTTTTCCCTCCCTTCTGAGGTGCAATGAGCGAGTCAATGAGCATCTCTAACTT 490

QY 2467 TGCATTTAGTTTTCAGTGAATGAGCTTTTAACTTCAATCCAGATCTCTATGCCAG 2526

Db 489 TGCATTTAGTTTTCAGTGAATGAGCTTTTAACTTCAATCCAGATCTCTATGCCAG 430

QY 2527 GTTGTCTGAGGTTAACTTTTGAAGTATATATACCTGCTTCTGCTATCTTATGTCATA 2586

Db 429 GTTGTCTGAGGTTAACTTTTGAAGTATATATACCTGCTTCTGCTATCTTATGTCATA 370

QY 2587 ACTCTGCGGTACAGTAATGAGATGATACCGGTACTTCCCTCCACACCATACGATA 2646

Db 369 ACTCTGCGGTACAGTAATGAGATGATACCGGTACTTCCCTCCACACCATACGATA 310

QY 2647 AAGCAAGCATTTTATACGATACCGAGTCACTATGTGTCCTCCCTGAAATTAACGAT 2706

Db 309 AAGCAAGCATTTTATACGATACCGAGTCACTATGTGTCCTCCCTGAAATTAACGAT 250

QY 2707 TCGAATCCATGCACTGAGTATATTTTCTAAGTTTGAAGTCTTCTTCTTTA 2766

Db 249 TCGAATCCATGCACTGAGTATATTTTCTAAGTTTGAAGTCTTCTTCTTTA 190

QY 2767 AAAAATATACAGCTTCACTAAATGATTTAGTCAGATTCCTAGATCGAAGAAC 2826

Db 189 AAAAATATACAGCTTCACTAAATGATTTAGTCAGATTCCTAGATCGAAGAAC 130

QY 2827 CTAACAAAAAATATTTTAAAGATATAAATATATGCTGTATATGTTATGTAATTTT 2886

Db 129 CTAACAAAAAATATTTTAAAGATATAAATATATGCTGTATATGTTATGTAATTTT 70

QY 2887 TAGGCTATATACATCTCTATTTTGGCATTTTCAATAAATGCTCTAAATACAAAAA 2945

Db 69 TAGGCTATATACATCTCTATTTTGGCATTTTCAATAAATGCTCTAAATACAAAAA 11

RESULT 15

LOCUS CB241863/C

DEFINITION UI-CF-FNO-aga-i-07-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone

ACCESSION CB241863

VERSION CB241863.1

KEYWORDS GI:28363507

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 726)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB

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Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).

The following repetitive elements were found in this cDNA sequence: 95-123, >AT rich#Low\_complexity (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

## FEATURES

Location/Qualifiers

1..726

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-CF-FNO-aga-i-07-0-UI"

/tissue\_type="Human Lung Epithelial cells"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-CF-FNO"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DUI). The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu

TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS

6hr to LPS 24h

TAG LIB=UI-CF-FNO

TAG\_SEQ=CTGCTCAGGT"

## ORIGIN

Query Match 24.3%; Score 715; DB 14; Length 726;

Best Local Similarity 100.0%; Pred. No. 5.8e-139;

Matches 715; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2231 GGGGAGCAACTGACATGGTTGAATGATAGCATTTCACTGCTTCTCTAGATCTGA 2290

Db 725 GGGGAGCAACTGACATGGTTGAATGATAGCATTTCACTGCTTCTCTAGATCTGA 666

QY 2291 GCAAGCTGTGCTTCTCACCCCGGCTGTATATACATGAGCTAACTTTTAAATGTC 2350

Db 665 GCAAGCTGTGCTTCTCACCCCGGCTGTATATACATGAGCTAACTTTTAAATGTC 606

QY 2351 ACAAAGCGCATCTCCAGATTCAGACCTCGCGCATGACTTTTCTGAGGCTTGCCTT 2410

Db 605 ACAAAGCGCATCTCCAGATTCAGACCTCGCGCATGACTTTTCTGAGGCTTGCCTT 546

QY 2411 TCCTCGCTTCTCTGAGGTGCGCATTAGAGCGAGTCACATGAGCATCTTAACCTTGA 2470

Db 545 TCCTCGCTTCTCTGAGGTGCGCATTAGAGCGAGTCACATGAGCATCTTAACCTTGA 486

QY 2471 TTTTAGTTTTTACAGTGAAGCTTAAAGTCTCATCGCATTTCTAATGCCAGTTG 2530

Db 485 TTTTAGTTTTTACAGTGAAGCTTAAAGTCTCATCGCATTTCTAATGCCAGTTG 426

QY 2531 CTGTAGGTAACCTTTTGAAGTATATATTTACCTGCTTCTGCTATCTTAGTCATAACTC 2590

Db 425 CTGTAGGTAACCTTTTGAAGTATATATTTACCTGCTTCTGCTATCTTAGTCATAACTC 366

QY 2591 TGGCGTACAGGTAAATGAGAAATGTACTACGGTACTTCCCTCCACACCATACGATAAGC 2650

Db 365 TGGCGTACAGGTAAATGAGAAATGTACTACGGTACTTCCCTCCACACCATACGATAAGC 306

QY 2651 AAGCATTTTATACGATACGATACGATGCTATGTTGCTTCTCCCTGAAATACGATTCGA 2710

Db 305 AAGCATTTTATACGATACGATACGATGCTATGTTGCTTCTCCCTGAAATACGATTCGA 246



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QY 2711 AATCCATGCAATGCAATATATTTTCTAAGTTTGGAAAGCAGGTTTTTTCCTTTAAAAA 2770
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245 AATCCATGCAATGCAATATATTTTCTAAGTTTGGAAAGCAGGTTTTTTCCTTTAAAAA 186
QY 2771 AATTATAGACACGGTTTCACTAAATTCAGTTAGTCAGAAATTCCTAGACTGAAAGAACCTAA 2830
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
185 AATTATAGACACGGTTTCACTAAATTCAGTTAGTCAGAAATTCCTAGACTGAAAGAACCTAA 126
QY 2831 ACACAAAAATATTTTAAAGATATAAATATATGCTGTATATGTTATGTAATTTTATAGG 2890
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
125 ACACAAAAATATTTTAAAGATATAAATATATGCTGTATATGTTATGTAATTTTATAGG 66
QY 2891 CTATAATACATTTCCCTATTTTTCGCAATTTTCAATAAAATGCTCTAATACAAAAA 2945
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
65 CTATAATACATTTCCCTATTTTTCGCAATTTTCAATAAAATGCTCTAATACAAAAA 11

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Search completed: April 25, 2004, 19:28:04  
Job time : 7366 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2004, 13:53:44 ; Search time 46 seconds  
(without alignments)  
3374.673 Million cell updates/sec

Title: US-09-978-188A-7

Perfect score: 2527  
Sequence: 1 MVKFPALHYWPLRFLVPL.....TDMPTTEVTDIVEMRENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2479	98.1	492	11 Q8C438	Q8C438 mus musculus
2	183.5	7.3	449	16 Q8YXP4	Q8YXP4 anabaena sp
3	180.5	7.1	453	16 Q8ZSC4	Q8ZSC4 anabaena sp
4	138	5.5	455	16 Q8XHF0	Q8XHF0 clostridium
5	121.5	4.8	474	2 Q9RHD4	Q9RHD4 pseudomonas
6	119.5	4.7	593	16 Q9JYN9	Q9JYN9 neisseria m
7	118.5	4.7	462	17 Q96YE7	Q96YE7 sulfobolus
8	118.5	4.7	490	17 Q8THQ1	Q8THQ1 methanosarc
9	117.5	4.6	511	16 Q8CNP2	Q8CNP2 staphylococ
10	117.5	4.6	693	16 Q9JTN5	Q9JTN5 neisseria m
11	117	4.6	450	16 Q8XT07	Q8XT07 ralsonia s
12	117	4.6	469	16 Q81F82	Q81F82 bacillus ce
13	117	4.6	481	2 Q9RQG9	Q9RQG9 streptococc
14	117	4.6	481	2 Q07870	Q07870 streptococc
15	117	4.6	535	6 Q9N1Q4	Q9N1Q4 oryctolagus
16	116.5	4.6	529	13 Q7ZWV7	Q7ZWV7 xenopus lae

```

17 115.5 4.6 670 8 021285 021285 reclinomona
18 115.5 4.6 784 16 Q8KDB0 Q8KDB0 chlorobium
19 115 4.6 444 16 Q8Y9Z4 Q8Y9Z4 listeria mo
20 115 4.6 507 16 Q8K9E2 Q8K9E2 bacillus ha
21 114.5 4.5 447 17 Q28801 Q28801 archaeglob
22 114.5 4.5 547 16 Q879H7 Q879H7 streptococc
23 114 4.5 542 16 Q8K673 Q8K673 streptococc
24 113.5 4.5 512 16 Q99SY5 Q99SY5 staphylococ
25 112.5 4.5 398 16 Q8Z4K9 Q8Z4K9 salmonella
26 112.5 4.5 488 16 Q891V9 Q891V9 clostridium
27 112.5 4.5 497 2 Q30986 Q30986 staphylococ
28 112 4.4 461 17 Q8U2X0 Q8U2X0 pyrococcus
29 111.5 4.4 559 16 Q8PJP2 Q8PJP2 xanthomonas
30 111 4.4 475 16 Q88XM1 Q88XM1 lactobacill
31 111 4.4 542 16 Q99YJ6 Q99YJ6 streptococc
32 111 4.4 556 16 Q8NZX7 Q8NZX7 streptococc
33 111 4.4 582 16 Q81F44 Q81F44 bacillus ce
34 110.5 4.4 400 16 Q8Z407 Q8Z407 salmonella
35 110.5 4.4 452 16 Q92FS0 Q92FS0 listeria in
36 110.5 4.4 826 16 Q88I00 Q88I00 pseudomonas
37 110 4.4 450 16 Q8E3W6 Q8E3W6 streptococc
38 110 4.4 599 10 Q7X9X8 Q7X9X8 plantago ma
39 109.5 4.3 400 16 Q8ZVA5 Q8ZVA5 salmonella
40 109.5 4.3 427 16 Q9KSI1 Q9KSI1 vibrio chol
41 109 4.3 412 16 Q88WH5 Q88WH5 lactobacill
42 109 4.3 450 16 Q8DYA1 Q8DYA1 streptococc
43 109 4.3 494 16 Q8KCP9 Q8KCP9 chlorobium
44 109 4.3 552 16 Q886F5 Q886F5 pseudomonas
45 108.5 4.3 450 16 Q8YAS9 Q8YAS9 listeria mo

```

#### ALIGNMENTS

#### RESULT 1

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ID Q8C438 PRELIMINARY; PRT; 492 AA.
AC Q8C438;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Progressive ankylosis.
GN ANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=hippocampus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK083135; BAC38778.1; -
DR MGD; MGI:86023; ank.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0007626; P:locomotory behavior; IMP.
DR GO; GO:0001501; P:skeletal development; IMP.
SQ SEQUENCE 492 AA; 54336 MW; 6923EA3A85D0BDC CRC64;

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Query Match 98.1%; Score 2479; DB 11; Length 492;

Best Local Similarity 97.8%; Pred. No. 1.6e-203;

Matches 481; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MVKFPALHYWPLRFLVPLGITNIAIDFGEQALNKGIAAKVEDAVEMLASYGIAVSLMK 60

Db 1 MVKFPALHYWPLRFLVPLGITNIAIDFGEQALNKGIAAKVEDAVEMLASKLDVSLMK 60

Qy 61 FFTGPMSEDFKNVGLVFNVNSKRDRTKAVLCMVVAGAIAAVPHTLIAYSDIGYIINKLHV 120

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Db 61 FFTGPMDSFKNVGLVFNYSKRDRAKAVLCMVVAGIAAFAHTIIAYSDLGYYIINKLHV 120
QY 121 DESVGSKTRRAFLYLAAPFPDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180
Db 121 DESVGSKTRRAFLYLAAPFPDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL 180
QY 181 HSHLECEPLIPILSLYMGALVRCCTTLCIGYYKNHDIIPDRSGPELGGDATIRKWSF 240
Db 181 HSHLECEPLIPILSLYMGALVRCCTTLCIGYYKNHDIIPDRSGPELGGDATIRKWSF 240
QY 241 WWPALILATORISRPVNLVFSRDLGSSAAEAVAILTATVPVGHMPPYGMWTEIRAVY 300
Db 241 WWPALILATORISRPVNLVFSRDLGSSAAEAVAILTATVPVGHMPPYGMWTEIRAVY 300
QY 301 PAFKNNPSKLVSTNTVTAHHKFTFVCMALSLTLCFVMTWPNVSKILLIDIGVD 360
Db 301 PAFKNNPSKLVSTNTVTAHHKFTFVCMALSLTLCFVMTWPNVSKILLIDIGVD 360
QY 361 FAFELCVPLRIEFPFPVTVRAHLLTGMWTKTFLVAPSSVRIIIVLASLVLPY 420
Db 361 FAFELCVPLRIEFPFPVTVRAHLLTGMWTKTFLVAPSSVRIIIVLASLVLPY 420
QY 421 LGVHGATLGVGLLAGFVGSSTWVAIAACVYVRKQKKMENESATEGEDSAMTMPTEE 480
Db 421 LGVHGATLGVGLLAGFVGSSTWVAIAACVYVRKQKKMENESATEGEDSAMTMPTEE 480
QY 481 VTDIVEMREENE 492
Db 481 VTDIVEMREENE 492

RESULT 2
Q8YXP4 PRELIMINARY; PRT; 449 AA.
AC Q8YXP4;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Hypothetical protein A111168.
GN A111168.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
  Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
  Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
  Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
  Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
  cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003584; BAB73125.1; -.
DR PIR; AE1952;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 449 AA; 49860 MW; F5841D2C1CC82D5 CRC64;

Query Match 7.3%; Score 183.5; DB 16; Length 449;
Best Local Similarity 21.0%; Pred. No. 3.5e-07;
Matches 97; Conservative 92; Mismatches 201; Indels 71; Gaps 14;

QY 13 LIRFLVPLIGITNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMKPFTGPMDS 68
Db 25 LTQFIPUSLSDVAMTLGDPLOTGALS- -LAFFQ- -ETLAGVGVKGVAVFLESFIIM 79
QY 69 FKNVGLFVFNKRDRTKAVLCMVVAGIAAFAHTIIAYSDLGYYIINKLHVDESVGSKT 128
Db 80 ILHASTALGGQAKSRRLAQFTIAGLVLSGIFLLTWEPLYNLLDVFVSSLSIAQRG 139
QY 129 REAFVLAAPFPDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLECRE 188
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Db 140 RTAFILMLFWPFVIAWRRFQGLLIRAQKSIAGWASVARLTWVVSLLVGVNURLDGM 199
QY 189 PLLIPILSLYMGALVRCCTTLCIGYYKNHDIIPDRSGP- - -ELGSDATIRKM- - -L 238
Db 200 LAGITWGAAILLEAVLTWFCG- - - - -RLGAISILEQGYSETKKLPQTLSGV 247
QY 239 SFWW-PIALIIATQIRSPIVNLVFSRDLGSSAAEAVAILTATVPVGHMPPYGMWTEI- 296
Db 248 SFYFLPLASTWLVWGAFRAILLIARSFDGSL- - -ALAVWPAT- - - -WGLLSIA 296
QY 297 - - - - -RAVYPAFPKNNPSKLVSTNTVTAHHKFTFVCMALSLTLCFVMTWPNVS 349
Db 297 NGRMIQOVVISAYEE- - - - -TSERTLAAFV- - - - -IIVGLSFTLIPEFLGFTDQG 342
QY 350 EKILIDIIQVDPAPAFELCVPLRIEFPFPVTVRAHLLTGMWTKTFLVAPSSVLR- - 407
Db 343 LFLLEQFTLGNPNLSVEASRPVLIQSLCPFLLIQNTFQGLLIHKKGNWFINLATVVAAT 402
QY 408 -IIVLIASLVLPYLGVHGATLGVGLLAGFVGSSTWVAIA 447
Db 403 FTLVLCGSLITKSGATSAAYG- - -MLAGVMSHIIIVFLA 440

RESULT 3
Q8ZSC4 PRELIMINARY; PRT; 453 AA.
AC Q8ZSC4;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Hypothetical protein A1r7587.
GN A1r7587.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
  Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
  Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
  Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
  Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
  cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003602; BAB77230.1; -.
DR PIR; AH2537; AH2537.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 453 AA; 49289 MW; 5E9337F924EE9B87 CRC64;

Query Match 7.1%; Score 180.5; DB 16; Length 453;
Best Local Similarity 20.4%; Pred. No. 6.4e-07;
Matches 94; Conservative 91; Mismatches 206; Indels 69; Gaps 15;

QY 13 LIRFLVPLIGITNIAIDFGEQALNRGIAAVKEDAVEMLASVGLAYSLMKPFTGPMDSFKNV 72
Db 34 LKQFIPUSLSDVAMTLGDPLOTGALSRLSPFQ-ETLAGVGVKGVAVFLESPIIMILHA 92
QY 73 GLVFNKSRDRTKAVLCMVVAG-ATAAVFHTLIAYSDLGYYIINKLHVDESVGSKTERRA 131
Db 93 STALGQAKSRRLVQFTVIAGLALSGIF-LFLTWKLYNNLLDLFGVSSSIAARGRTA 151
QY 132 FLYLAAPFPDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLE- - - 185
Db 152 FLMLFWPFVIAWRRFQGLLIRAQKSIAGWASVARLTWVVSLLVGVNURLDGAFLAG 211
QY 186 - - - - -CREPLIIPILSLYMGALVRCCTTLCIGYYKNHDIIPDRSGPELGGDATIRKWL 238
Db 212 ITWMGAILLEAVLTWFCGRLGAISILNQ- -QGYSET- - - - -KKLPQTGEVTF- - - 258
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QY	239	STWWPDLIALIATQIRISRPINVLNFSVRDLGGSSAATENAVAILTATYVPGHMPYGMWLTET	290
DB	259	-YYLPLASTMIIWVGARAILLSLTARAFDGS-----IALAWPAA-----WGLLSIAN	306
QY	297	-----RAVYPAFDCKNPSNKLVTSTNTVTAHHKKFTFVCMALSLTLCFVWFMTPNYSE	350
DB	307	GTRMTQQVVISAYEE-----TSRRTLAAFV-----IIVGLSFTLIPFFLGYTDOGL	352
QY	351	KILIDIIIGVDFAFELCVVPURISFPFVPTVRAHLTGWLMTL-KKTFFVLAPSSVLRII	409
DB	353	FLTROFLGNPNPSLVNASRPFVQILSCLPLLLALQNTFQGLLIHKGNWFINTATLVAIL	412
QY	410	VLI--ASLVNLPYLGVGHGATLGVGSLLAGFVGSESTVAIA	447
DB	413	TLIVVGTLLIFTHSGANSAAVG---MLAGVIGEIIIVLFFA	449
RESULT 4			
QBXHF0	ID	QBXHF0	PRELIMINARY; PRT; 455 AA.
AC	QBXHF0		
DT	01-MAR-2002	(TrEMBLrel. 20, Created)	
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Hypothetical protein CPB2535.		
GN	CPB2535		
OS	Clostridium perfringens.		
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;		
OC	Clostridium.		
ON	NCBI_TaxID=1502;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=13 / Type A;		
EX	MEDLINE=21664373; PubMed=11792842;		
RA	Shimizu T., Ohcuni K., Hirakawa H., Ohshima K., Yamashita A.,		
RA	Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;		
RT	"Complete genome sequence of Clostridium perfringens, an anaerobic		
RT	flesh-eater;"		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).		
DR	EMBL; AP003194; BAB82241.1;		
DR	GO; GO:0016020; C.membrane; IEA.		
DR	GO; GO:0015297; F:antipporter activity; IEA.		
DR	GO; GO:0015238; F:drug transporter activity; IEA.		
DR	GO; GO:0006855; P:multidrug transport; IEA.		
DR	InterPro; IPR002528; Mate.		
DR	Pfam; PF01554; Mate; 2.		
DR	TIGRFAMs; TIGR00797; mate; 1.		
KW	Hypothetical protein; Complete proteome.		
SQ	SEQUENCE	455 AA; 46984 MM; A564CC4F22FBD059 CRC64;	
Query Match			
Best Local Similarity 21.0%; Pred. No. 0.0028;			
Matches 97; Conservative 82; Mismatches 190; Indels 94; Gaps 19			
QY	17	LVPLGIT-NTAIDFGQALNRGIAAYKEDAVEMLASYGSLVSMKFFFTGPSDFKNVGLV	75
DB	71	LIGIGATNISIKFGQNK-----RKQAEKILGNVLLITISLV-----ITVIGIV	116
QY	76	FVNSKRDRTKAVLCWVAGAAIAVFHTLIAYSDLYIINKLHVDESVGSKTRAFLYL	139
DB	117	PANS-----ILHLFGASEATIFV--AKEVINVLIGITFNLMSPSLYSTIRA----	161
QY	136	AAFPFMDAMWTHAGILLKHKYFELVGCASISDVIAQVFAILLHSHLECEELIPIL	198
DB	162	DGNPKMSAAV-----MWLGC--IINVLDVAFIVFV--NLGKGAALATVI	203
QY	196	SLYNGALVRCTTLCGLYKKNHIDIIIDRSPELGGDATRKMLSF--WWPLALILA----	244
DB	204	SQIV-----TTLIMLYYT-----LGSNKLKFKETKLDWLKVLKIVLAIGV	249
QY	250	---TQRISRPINLVFSRDIG--GSSAATENAVAILTATYVPGHMPYGMWLTETRAVPADF	306
DB	246	APFSNMAASVVOVIANNALRMVGGDILAIGAMAIISSIAMIFLMPITGQ--GSQPTIG	303

305 KNPSKLVSTNTVTAHKKFTFCVMSALSLTLCFWMFTWPNVSEKILLDILIGVDFAFA 364

304 YNGAKYERAKQVKLMAIAATLVLGILLQAF-----PALVISMNSDPKLL 354

365 ELCWPLRIFSPFPVTVRAHLTGMIMTKTKFTVLAPSVLR-IIVLIASLVLPVLGV 423

355 EICVPGRLIVFWPIIGISIIIGSNYFQSIGKAKLATFSLLRQVILLIPLTLVLPKIAG 414

424 HGATLGVSLLAGFVGEISTVAIAACVYVRKQKK--MENESA 464

415 LGLT--GWLAGTVSDFSLTITGLFIKEFKEDSIEDEKA 454

RESULT 5

Q9RHD4 PRELIMINARY; PRT; 474 AA.

AC Q9RHD4;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Wzx (Similar to polysaccharide biosynthesis protein).

OS WZX.

GN Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI\_taxid=287;

LN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=IATS O6;

RC MEDLINE=20090474; PubMed=10627048;

EX Belanger M., Burrows L.L., Lam J.S.;

RA "Functional analysis of genes responsible for the synthesis of the B-

RT band O antigen of pseudomonas aeruginosa serotype O6

RT lipopolysaccharide";

RT Microbiology 145:3505-3521(1999).

LN [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=22053227; PubMed=12057956;

RX Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutyavvin T.V.,

RA Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.;

RT "Genetic Variation at the O-Antigen Biosynthetic Locus in Pseudomonas

RT aeruginosa";

RL J. Bacteriol. 184:3614-3622(2002).

LN [3]

RN SEQUENCE FROM N.A.

RC STRAIN=2-164;

RA Spencers D., Kas A., Smith E., Raymond C., Sims E., Hastings M.,

RA Burns J., Kaul R., Olson M.;

RT "Whole Genome Sequence Variation Among Multiple Isolates of Pseudomonas

RT aeruginosa";

RL J. Bacteriol. 0:0-0(2003).

DR EMBL; AF035937; AAF24000.1; -

DR EMBL; AF498417; AAM27819.1; -

DR EMBL; AF540991; AAO17416.1; -

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.

DR InterPro; IPR002797; Polysacc synt.

DR Pfam; PF01943; Polysacc synt; 1.

SQ SEQUENCE 474 AA, 51401 NW, C867BC84E086E1B6 CRC64;

Query Match 4.8%; Score 121.5; DB 2; Length 474;

Best Local Similarity 20.3%; Pred. No. 0.075;

Matches 89; Conservative 75; Mismatches 174; Indels 101; Gaps 21

QY 48 MLASGLAYSLMKFTGPMSPDKNGL-VFVN--SKRDRTKAVLCWVAGAAVPHTLI 104

Db 1 MLGKSLVYVLFKSPAIL--LVGLSVFTLLSPGEYGVYSLTIIVGFLNVTFLQW 57

QY 105 AYSDIGYIYINKLHVDSVGSK---TRAFYLAAFP--FMDAMAW---THAGI-LLKH 155

Db 58 ALG-VGRYL---PECSDDQARALGTATISFLVSLVITVFTFLWREIGISILYY 113

	Query Match	Best Local Similarity	Matches	4.8%;	Score 121.5;	DB 2;	Length 474;
		20.3%;	Pred. No. 0.075;				
		89;	Conservative	75;	Mismatches	174;	Indels 101; Gaps 21
QY	48	MLASVGLAYLMKFTGPMSPDKNVL-VFVN--SKRDRTKAVLCWVAGAAVFEHLI	104				
DB	1	MLGKSLVYLFKSPAILT--LVGLSVFTLLSPGEYGVYSLTIIVGVFLNTVFLQW	57				
QY	105	AYSDDLGYIINKLHVHDSVGSK--TRRAFLYLAAFP--FMDAMAW---THAGI--LLKH	155				
DB	58	ALG-VGRYL--PECSDDQARALGTARISLVSILVIPTFLWEHREIGSILYY	113				

156 KYSFLVGCASISD-----VIAQVVFVAILHSHLEPRELLIPILSYMG----- 200  
114 MVSFLCLAQWHLNLKIONAILQPLTYGKMLL---IKGAGSFFIGVLLVYFGVGDGLL 170  
201 -----ALVRCCTTCLGYYKXNHDIIIPRSQPELGGDATIRKMLSFWEPLALILATORISR 255  
171 LGTVLSVLAVITFQDAWRGVSVALVDKE-----QLTRLFAYGAPLTLTFLFAFYVN 222  
256 PIVNLFYSRDLGGSSAATEAVAILTATYPVG-----HMPYGMWLTETRAYVPAPDKNPS 309  
223 ASDRFFIGAFGLGDAAGVYSVSYDLAQVSGTVASVVHLL-----AAFLVMKLSK 273  
310 NKLIVSTNTVTAHKKFTFCVMALSLTLCFVMTWPNVSEKILIDIIGVDEFAFAELCVV 369  
274 SGLPQTQDLR---KTFIFAVVSPACGLAWVAEISGSIN-----GEFFREGALKII 325  
370 PLRIFSPFPVTVRAHLTGLWMTIKK-----TFVLAPSSVLRIVLIAS-----LV 416  
326 PL-----ISLSAFLGALKSPFYDYSFQLASATRVQVTVAVSAVVDWENLI 372  
417 VLPYLGVGHGATLGVSLLA 435  
373 LIPEFGIVGA--AVSSVMA 389

RESULT 6  
Q9JYN9 PRELIMINARY; PRT; 693 AA.  
AC Q9JYN9;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
DE Carbon starvation protein A.  
GN NMB1493  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=491;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC58 / Serogroup B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
RA Eisen J.A., Ketchum K.A., Hood D.W., Feden J.F., Dodson R.J.,  
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,  
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,  
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,  
RA Gill J., Scarlato V., Maignani V., Pizze M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58."  
RL Science 287:1809-1815(2000).  
DR EMBL; AE002498; AAP41849.1; -.  
DR PIR; C81078; C81078.  
DR TIGR; NMB1493; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0009267; P:cellular response to starvation; IEA.  
DR InterPro; IPR003706; CstA.  
DR Pfam; PF02554; CstA; 1.  
KW Complete proteome.  
SQ SEQUENCE 693 AA; 74518 MW; A315785B6985DC0 CRC64;

Query Match 4.7%; Score 119.5; DB 16; Length 693;  
Best Local Similarity 22.2%; Pred. No. 0.18; Indels 139; Gaps 26;  
Matches 111; Conservative 69; Mismatches 181; Indels 139; Gaps 26;

12 PLIRFLVPLGTTNIAIDFGS-QALNRGIAAVKSDAVEMLASYLGLAYSLMKFFGPMSPDK 70  
270 PVMLLLPDYLSLTFLLGTTIAALGLIVV-NPALQMPAVTHFDGSGVFSGALFPF- 327  
71 NVGLVFNKSDRTKAVLCMVAGAAVPHLLIAYSDLGYYIINKLHVDESQSKTR 130

328 -----LPI-----TIACGAVSG-----PHALISGTTPKOLENETHVRMIGYGMIME 370  
131 AFLYLAAFPFNDAMWTHAGI-LLKHKYSFLVGCASISDVIAQV-----VFVAILLH 181  
371 SFVAIMA---LAAASLDPPGYFAKNSPALIG---TDANTAAEVITTKLQFPVDAAILLH 425  
182 SHLECREPLLPILSLYMGALVRCCTTCLGYYKXNHDIIIPRSQPELGGDATIRKMLSF 241  
426 TAKEVGEN---TILSRAGA---PTLAVGMAHIMSLIP-----GEA---MMAFW 466  
242 WPLAIL-----ATQISRPVNLFVSRDLGG-----SSAATEAVAILTAT 282  
467 YHFALLFEALFILTAVDAGRVAR-----FMQDLGSIFFYKPGNTDSIPANLIATFFAV 521  
283 YPVGHPYGMWLT-----IRAVYPAPDKNPNKLVSTNTVTAHKKFTFCVMALSLT 338  
522 ALWGFYLTGVTDPGLGINSWPLP-----GIANQMLA-----GVALIM 560  
339 CFVWF-----WTPNVSEKILIDIIGVDPAPFAELCVPLRIFSPFPVTVPAHLTG 389  
561 CAVVLIKMKRDYVWV-----VLVPAGVFLV---TCYAGIQKLFHSDPRISFHAHAGK 611  
390 WLMTLKKTFLAPS-----SVLRII-----VLIASLVLPYLGVGHGATLGVSLLA 435  
612 YSDALAKNEILAPAKDIGEMAQIIIFNDKINAGLTILFLSVVVI---VAAYGLRT---ALKA 666  
436 GFVGESTMVAIAACYVYRKQ 455  
667 RKVGWPTAKEIPAVYRDGKQ 686

RESULT 7  
Q96YE7 PRELIMINARY; PRT; 462 AA.  
AC Q96YE7;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
DE Putative NADH-plastoquinone oxidoreductase subunit 2.  
GN ST2223.  
OS Sulfolobus tokodaii.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=111955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JCM 10545 / 7;  
RX MEDLINE=21456156; PubMed=11572479;  
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,  
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,  
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
RA Oshima T., Kikuchi H.;  
RT "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain 7."  
RL DNA Res. 8:123-140(2001).  
DR EMBL; AF000989; BAB67330.1; -.  
DR GO; GO:0008137; P:NADH dehydrogenase (ubiquinone) activity; IEA.  
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u...; IEA.  
DR InterPro; IPR001064; Crystallin.  
DR InterPro; IPR001750; Oxidored\_qi.  
DR Pfam; PF00361; oxidored qi; 1.  
DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 462 AA; 50002 MW; E99467D221AE3892 CRC64;

Query Match 4.7%; Score 118.5; DB 17; Length 462;  
Best Local Similarity 19.0%; Pred. No. 0.13; Indels 127; Gaps 18;  
Matches 82; Conservative 78; Mismatches 145; Indels 127; Gaps 18;

69 FKVGLVFNKSDRTKAVLCMVVA-GAIAAVPHLLIAYSDLGYYIINKLHVDESQSK 127

Db 17 PSSIAVLIDN-GRSRYIIA VDLISIGTLVSLFLTLIFVGLGY- -----GYS 63  
 QY 128 TRAFLYIAAPFMDAMWTHAGILKKHYSFLVCCASISDVIAQVFAVAILLHSHLECR 187  
 Db 64 LFSSTLYLSNFGYFIA-----VSAILATI-----IVYGGMESL 97  
 QY 188 ELLIPILSLYMGALVRCTTLCGYKYNHDIIPDRSGPELGGDATIRKMLSFWMPLALI 247  
 Db 98 EPIKTRSFSLAMTDLGVIVLFAYSVII-----LASM----- 133  
 QY 248 LATQIRSPVNLVFSRDLGGSSAATEAVAILTATYP-----VGHMPYGWITERAV--Y 300  
 Db 134 -----GIASAATYVIAMIRKDYSTIAGVKYLINGLLSSLMVLGF 174  
 QY 301 PAFDKNPNKLVSTNTVTAAHIKFTFVCMALSLTLCF-----VNFWTPNV---SEK 351  
 Db 175 AFFILIGLSLDATINVTLVILG-----INFLSIAFLFKVGAFFQAWLPDYVNSDR 229  
 QY 352 ILI-----DIIGVDFAPAEIC-----VPLRIFSPFPVPTVRAHLTGWMLTKK-- 396  
 Db 230 ISVAFVSSVGKIVGIAPLFDIIYFLKPSGIVGFSIFVIFAL-ITVMSLIFGNIVAFSRQD 288  
 QY 397 -TFVLAPSSVRLIIVLIASLVLPYLGVHGTGLVGSLLAGFVGESTVVAIAACYVRKQ 455  
 Db 289 FASMLAYSSITQVGFMLIAITMLPY-----NPIVSTSGLMVYLAYS--IAQAGLFIALSH 342  
 QY 456 KKKMENESATEG 467  
 Db 343 IEKVSTSVIEG 354

## RESULT 8

ID Q8THQ1 PRELIMINARY; PRT; 490 AA.  
 AC Q8THQ1  
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Polysaccharide biosynthesis protein.  
 GN MA4461.  
 OS Methanosarcina acetivorans.  
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2214;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;  
 RX MEDLINE=21929760; PubMed=11932238;  
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,  
 RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atncor D., Brown R.,  
 RA Allen N., Naylor J., Strange-Thomann N., Dearellano K., Johnson R.,  
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,  
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,  
 RA Hederich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,  
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,  
 RA Springer T.A., Umayal L.F., White O., White R.H., de Macario E.C.,  
 RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,  
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,  
 RA Metcalf W.W., Birren B.;  
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic  
 RT and physiological diversity."  
 RL Genome Res. 12:532-542(2002).  
 DR EMBL; AE011167; AAM07802.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:000271; P:polysaccharide biosynthesis; IEA.  
 DR InterPro; IPR002797; Polysacc\_synt.  
 DR Pfam; PF01943; Polysacc\_synt; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 490 AA; 54715 MW; 03E2B2A3A9A0DB1 CRC64;

Query Match 4.7%; Score 118.5; DB 17; Length 490;  
 Best Local Similarity 22.1%; Pred. No. 0.14;  
 Matches 105; Conservative 82; Mismatches 158; Indels 131; Gaps 26;

QY 16 FLVPLGITNI--AIDFGEQA-LNRGIAAVKEDAVEMLASYGLAYSIMKFFTPGMSDFKNV 72  
 Db 27 FLPLV-ITKLGAYDGIWAQIN-----ITVSLVSPALMGLMSPIR----- 68  
 QY 73 GLVFNKSKDRKAVLCMVVAGNAIAVFTLAYSGLGYIINKLHHVDESVGSKTRRAF 132  
 Db 69 ---FLSETEKKK-----IREVYSILFFVTVSGFLASSLLYVFAEP----- 107  
 QY 133 LYLAAAPFMDAMA--WTHAGILKKHYSFLVGCASISDVIAQVFAVAILLHSHLECR-- 188  
 Db 108 --LATGFQDPSATYFVQAGSL-----IFLVIESIS-LFYPRVPRQIKKFSYFTLFTF 160  
 QY 189 -PLILPILSYMG-----ALVRCITCLG-----YKNHDIIPDRSGPELGGDATI 234  
 Db 161 GKLLFTLIFLMGYSGLLVITATLAVQGLIFLIAFTVIVSQIGFVIPQFT-----CI 212  
 QY 235 KXMLSFWPLA---LILATQIRSRPVLNLFVSRDLGGSSAATEAVAILTATYPVGHMPY 290  
 Db 213 REHLQSLPLTPNVLRWVTDSSDRYVTVFLG--LG-----SVGVYSAACSIGNLIQ 263  
 QY 291 GWLTERAV-YP---AFDQNPNSKLVSTNTVTAHKKKFTFVCM-----ALSLTL 338  
 Db 264 LFVSPQLILFPELSKLFDENKTDEVRIYMSHS-----LRYFLIIAIPAVFGLSALKPL 318  
 QY 339 CFVWFVTPNVSEKTLIDIGVDFAPAEICVVPVLRIFSPFVPTVRAHLTGWMLTKTF 398  
 Db 319 LGVLTQDFVSGWVFVPII---AFAGLLVGIFQIF-----VNTFLIKKT- 360  
 QY 399 VLAPSSVLRIRVILIA-----SLVPLVYLGVHGTGLVGSLLAGFVGESTVVAIAACY 450  
 Db 361 --RPATVINILAAVSNVLINLILIPSVGIAAGAL--STLVSYFLMAALCMRVTLKY 412

RESULT 9  
 ID Q8CNP2 PRELIMINARY; PRT; 511 AA.  
 AC Q8CNP2  
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE High affinity proline permease.  
 GN SE1587.  
 OS Staphylococcus epidermidis.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 12228;  
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE016749; AAO05186.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005215; P:transporter activity; IEA.  
 DR GO; GO:0008810; P:transport; IEA.  
 DR InterPro; IPR001734; Na/solut\_sympor.  
 DR Pfam; PF00474; SSF; 1.  
 DR TIGRFAMs; TIGR00813; sss; 1.  
 DR PROSITE; PS0283; NA\_SOLUT\_SYMP\_3; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 511 AA; 56025 MW; 2028D63BA046A568 CRC64;

Query Match 4.6%; Score 117.5; DB 16; Length 511;  
 Best Local Similarity 19.7%; Pred. No. 0.18;  
 Matches 93; Conservative 78; Mismatches 147; Indels 153; Gaps 22;

QY 53 GLAYSIMKFFTPGMSDFKNVGLVFNVSKDRDKAVLCMVVAGNAIAVFTLAYSGLGY 112  
 Db 117 GDAITLPDFKRLDDKNI-----IKISGLIIVVFPTL--YTHSGFV 158  
 QY 113 IINKLHHVDESVGSKTRRAFVLAAPFPMDAMWTHAGILKH-----KYSFLVG--CASI 166

Db 159 -----SGGK-----LFESAFGLN-----YHAGLLIVAIIVIFVTFPGYLAVSI 197  
 Qy 167 SDVIAQVFAVAILHSHLECEPELIPILSLYMGALVRCCTLCGYKYNTHDIIPDR-SG 225  
 Db 198 TDFQGVIMLIAM-----VWNPVIAL-----LKGWMDTFHDIAQMKPTN 237  
 Qy 226 PELGGDATIRKMLS-FWMLALILATORISRP-IVNLFVS-----RDLGGSSAAT 273  
 Db 238 LDLPFRGTIVGLVSLFSGLYG-----FGQPHIIVRFMSIKSHKLLPKARRLG---ISW 288  
 Qy 274 EAVAILTATYPVGHMPYCWLT-----IRAVYPAEDKNNPSKLVSTNTVTAHHIKFTF 329  
 Db 289 NAVGLLGA-IGVGLTGISFISERHIKSDPDLFVMSQILFHLPLVGGFLAAILAAMS 347  
 Qy 307 NPSKLVSTSTVT-----AAHIKKEFTFV---CMALSLLTLCFVMEFTNVSE 350  
 Db 348 TISSQLLVTSSTLDFYKLIRGSDKASHQKFEVLIGRLSVLLVAIVAITIAHPN--- 404  
 Qy 351 KILDIIGVDAFAELCVVPLRISEFFPVVYVAHITGMLTMTKFTVLAPSVLRIV 410  
 Db 405 DTILNLGVNAGGAAPSLVLSYWKDLTRAGASG-----MVAGAVV 450  
 Qy 411 LIASLVPLVGLVGGATVGSLLAGFVGESTMVAIAACVYVRKOKKMMEN 461  
 Db 451 VIVWISWIKPLATINAFPGWYEIIPGRI-----ISVLITIVSKLTKKPPD 496

## RESULT 10

Q9JTN5 PRELIMINARY; PRT; 693 AA.  
 AC Q9JTN5;  
 DT 01-OCT-2000 (TREMELrel. 15, Created)  
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
 DE Putative integral membrane protein (CstA-like).  
 GN NMA1698.  
 OS Neisseria meningitidis (serogroup A).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=656599;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=22491 / Serogroup A / Serotype 4A;  
 RX MEDLINE=20222556; PubMed=10761919;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrall B.G.  
 RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491."  
 RL Nature 404:502-506(2000).  
 DR EMBL; AL162756; CAB84926.1; --  
 DR PIR; E81865; E81865.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0009267; P:cellular response to starvation; IEA.  
 DR InterPro; IPR003706; CstA.  
 DR Pfam; PF02554; CstA; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 693 AA; 74545 MW; 1FID706269C20E46 CRC64;

Query Match 4.6%; Score 117.5; DB 16; Length 693;  
 Best Local Similarity 22.3%; Pred. No. 0.26;  
 Matches 100; Conservative 63; Mismatches 149; Indels 137; Gaps 24;  
 Qy 62 FTGPMDSFKNVGLVFNVKRDRTRKAVLCWVAGAAVAFHTLIAYSDLVGYIINKLHVD 121  
 Db 320 FSGALFFP-----LPI-----TIAGVSG-----FHAISSGTPKMLENETHVRM 361  
 Qy 122 EVSGKTRAFVLYLAAPFMDAMANTHAGI-LLKHYSFLVGCASISDVIAQV----- 173  
 Db 362 IGYGGLMESFVAIMA---LAAAASLDPGVYFAMNSPAALIG--TDANTAETVITTKLQF 416

Qy 174 -VFVAIIHSHLECEPELIPILSLYMGALVRCCTLCGYKYNTHDIIPDRSGPGLGDA 232  
 Db 417 PVDAATLHTAKEVEN---TILSRAGGA-----PTLAVGMAHIMSRLIP-----GEA 461  
 Qy 233 TIRKMLSFWMPLALIL-----ATQISRPVNLFVSRDLGG-----SSAAT 273  
 Db 462 ----NMAFWYHPALLFEALFILTAVDAGTRVAR-----FMQDLGSIYFKPFGNTDSIPA 512  
 Qy 274 EAVAILTATYPVGHMPYCWLT-----IRAVYPAEDKNNPSKLVSTNTVTAHHIKFTF 329  
 Db 513 NLIATFFAVALMGYFLYTCGTDPLGGINSWPLF-----GIANQMLA----- 554  
 Qy 330 VCMALSLLTLCFYMF-----WTPNVSEKILIDIIGVDAFAELCVVPLRISEFFPV 380  
 Db 555 ---GVALINCVAVLIMKRDYVWV-----VLVPAVGVLV---TCYAGLQKLFHSDPR 602  
 Qy 381 VTVRAHLTGWMLTKKTFVLAPS-----SVLRIT-----VLIAISLVLPVGLVHGA 426  
 Db 603 ISFLAHTGYSDALAKNEVLPAKDIGEMAQIIFNDKINAGLTILFLSVVVI---VAATGL 660  
 Qy 427 TLGVGSLLAGFVGESTMVAIAACVYVRKQ 455  
 Db 661 RT---ALKARKVGWFTAKEIPAVYRDGKQ 686

## RESULT 11

Q8XT07 PRELIMINARY; PRT; 450 AA.  
 AC Q8XT07;  
 DT 01-MAR-2002 (TREMELrel. 20, Created)  
 DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Probable macrofide-efflux transmembrane protein.  
 GN RSP0310 OR RS05460.  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GMI1000;  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.  
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum."  
 RL Nature 415:497-502(2002).  
 DR EMBL; AL646078; CAD17461.1; --  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000524; HTH GntR.  
 DR InterPro; IPR007114; MFS.  
 DR PROSITE; PS00043; HTH GNTX\_FAMILY; 2.  
 DR PROSITE; PS00850; MFS; 1.  
 KW Plasmid; Complete proteome.  
 SQ SEQUENCE 450 AA; 46773 MW; 4F3715370BA4E5A6 CRC64;

Query Match 4.6%; Score 117; DB 16; Length 450;  
 Best Local Similarity 20.8%; Pred. No. 0.17;  
 Matches 100; Conservative 70; Mismatches 186; Indels 124; Gaps 19;  
 Qy 29 FGEQALNRGIRAAVKE-----DAVELASVGLAYSLMKFTGPMDSFKNVGLV 77  
 Db 53 FGQALSLGSLTGTGVLWMTDTTGSVALATAGLALL-----POAVLSPUGTFA 106  
 Qy 78 NSKRDTRKAVLCWVAGAAVAFHTLIAYSDLVGYIINK--LHHVDESVGSKTRAFVLY 135

Db 107 -----DRYSRRLMIVADGISALCMLLL-----IALFLTGRIALMHWAYVMMAIRS----- 151  
 QY 136 AAFPNDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILLHSHLECREPILIPIL 195  
 Db 152 AAQAFAPAA--AASVTVLPGFVRAAGINOSLSLTLV-----VAAPLG 196  
 QY 196 SLVWGA-----VRCTTLCGYKXNHHIIPD-----RSGPELGSDATIRKMLSFWP-- 243  
 Db 197 ALAIGVMPIGWALGIDVATALLGIAPLLCCRIPOACVSSGQKTGLMPAFREGVDLVWKTTP 256  
 QY 244 -----LALILATQIRSRPIVNLVFSRDLGSSAATEAVALLTATVPVGHMPYGLWTE 295  
 Db 257 GLRWLVLCGAVVLTIMPFTLVPLVKTHFGGAAA---QVALMEGLSIGWVAGLL-- 311  
 QY 296 IRVYPAFDKNPSKNLVSTNTVTAHHIKFTFVCMALSLLT-----CFVMPFTPN 347  
 Db 312 VAAMAP-----RQVAVILCGFAMSCVALALTALAPGSLFGVAVAMVW-- 354  
 QY 348 VSEKILLIDIIGVDFAPAEELCVPLRFSPFPVTVRAHLTGWMLTKKTFV-LAPSSVL 406  
 Db 355 -----ISGITVFVGNAPTAL-----LQTVPNHLOGRVLSLLNTTWGLAAPVGL 399  
 QY 407 RIIVLASLVPLVYLGVHGATLGVSLLAGFVGESTWVAIAACYVYRKOKKXWENESATE 466  
 Db 400 ALFTPLGEVIGVRAIFAIAGLLGAASLAGFLSPSLM-----RLDRPFSRSEARTD 450

## RESULT 12

Q81F82 ID Q81F82 PRELIMINARY; PRT; 469 AA.  
 AC Q81F82;  
 DT 01-JUN-2003 (T-EMBLrel. 24, Created)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE N4+ driven multidrug efflux pump.  
 GN BCI1716.  
 OS *Bacillus cereus* (strain ATCC 14579 / DSM 31).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 OX NCBI\_TaxID=226900;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22608415; PubMed=12721630;  
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,  
 RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,  
 RA Chu L., Mazur M., Goleman E., Larsen N., D'Souza M., Walunas T.,  
 RA Grechkin Y., Pusch G., Haselkorn R., Ponstein M., Ehrlich S.D.,  
 RA Overbeek R., Kyrpides N.;  
 RT "Genome sequence of *Bacillus cereus* and comparative analysis with  
 RT *Bacillus anthracis*.";  
 RL Nature 423:87-91(2003).  
 DR EMBL; AE017003; AAP08692.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0015297; F:antipporter activity; IEA.  
 DR GO; GO:0015238; F:drug transporter activity; IEA.  
 DR GO; GO:0006855; P:multidrug transport; IEA.  
 DR InterPro; IPR002528; MatE.  
 DR Pfam; PF01554; MatE; 2.  
 DR TIGRFAMs; TIGR00797; matE; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 469 AA; 51613 MW; 1B831E84AE4231C CRC64;

Query Match 4.6%; Score 117; DB 16; Length 469;

Best Local Similarity 20.2%; Pred. No. 0.18;

Matches 98; Conservative 81; Mismatches 215; Indels 90; Gaps 20;

QY 16 FLVPLGNTIAID-----FGQALNRGIAA VKDAVEMLASYGSLMKFFFTGPMSEDFK- 70  
 Db 31 FLVPLLSNLVLSVGQFGVGVVGVWGLGV--NDLAAISAFFPLFLVSVFVIGSGSSI 88  
 QY 71 NVGLVFNKSRDRTKAVL-----CMVAGAAVAFHTLIAYSDLGYY-----IINKLHV 120  
 Db 89 LIGQAFGAKNEDRLKAVGTTLFTFTFIGVLLAIGSIFAMIRLMGTPENIIESVHY 148

QY 121 DESVGSKTRAFPLYLAAFPFMDAMAWTHAGILLKHYSFLVGCASISDVIAQVVFVAILL 180  
 Db 149 ARILFISMPVFLYFAVTTMRGTGDS-----KTPYFLIVSTALN-----MILLPILI 197  
 QY 181 HSHLECREPILIPILSLVWGAALVRCTTLCGYKXNHHIIPDRSGPELGSDATIRK----- 236  
 Db 198 FGNLGA-----PKLDVYGAAYASVISTVITFVYL--VYLKKQHPLQDGTVRKYLRLM 249  
 QY 237 -----MLSFWMPLALILATQIRSRPIVNLVFSRDLGSSAATEAVAILTATVPVGHMP 289  
 Db 250 DGEILLKULLRIGIPASINMLIVLSLSEIAVAFVNR-YGSDATAAYGVVNVQVASV--QMP 306  
 QY 290 YGWLTVETRAVPAFDKNPSKNLVSTNTVTAHHIKFTFVCMALSLLTLCF-----VWFV 344  
 Db 307 AVSLGITVSIFAA--QSIGANQFDRLOKVVKAGIMNYVIGGVLLISLYVFSRDLSLFL 364  
 QY 345 TPNVSEKILLIDIIGVD-----PFAELCVPLRFSPFPVTVRAHLTGWMLTKKTF 398  
 Db 355 TSQTTIEAHSLVMTLWSYLIFGHAQI-----ISATRASGT----- 402  
 QY 399 VLAPSSVLRIIVLASLVPLVYLGVHGATLGVSLLAGFVGESTWVAIAACYVYRK--Q 455  
 Db 403 VLWPTVIGVWSIMLVEVPVAYLSYH-TSLGIEGIGWGYPA-APIVSLILQYAYYKLSWQ 460  
 QY 456 KKQM 459  
 Db 461 KKRI 464

## RESULT 13

Q9RQ9 ID Q9RQ9 PRELIMINARY; PRT; 481 AA.  
 AC Q9RQ9;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Putative oligosaccharide repeat unit transporter.  
 GN CPS19CJ.  
 OS *Streptococcus pneumoniae*.  
 OC Bacteria; Firmicutes; Lactobacillales; *Streptococcaceae*.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99395043; PubMed=10464207;  
 RA Morona J.K., Morona R., Paton J.C.;  
 RA "Comparative genetics of capsular polysaccharide biosynthesis in  
 RT *Streptococcus pneumoniae* types belonging to serogroup 19.";  
 RL J. Bacteriol. 181:5355-5364(1999).  
 DR EMBL; AF105116; AAD19923.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.  
 DR InterPro; IPR002797; Polysacc synt.  
 DR Pfam; PF01943; Polysacc synt; 1.  
 SQ SEQUENCE 481 AA; 53798 MW; 4FBCCCBF43CBBDAE CRC64;

Query Match 4.6%; Score 117; DB 2; Length 481;

Best Local Similarity 21.2%; Pred. No. 0.19;

Matches 102; Conservative 85; Mismatches 135; Indels 158; Gaps 30;

QY 4 FPALTYWPLI-RELVP--LQITNIAIDFGQALNRGIAA VKDAVEMLASVGLAYSLMK 60  
 Db 23 PFLIT--FPYISRLNPNIGLTFSSISG----NYGI-----LLASLGI----- 61  
 QY 61 FFTGPMSPKFNKVLGVFNNSKEDRTKAVL--CMVAGAAVAFHTLIAYSDLGYYIINKLH 118  
 Db 62 -----STYGIKAVASVREDRDKLSKVQELMIINVAISIITALLFMTI---FITQLN 112  
 QY 119 HVDESVGSKTRAFYL-----AAPFDMAWTHAGILLKHYSFLVGCASISDVIA 171  
 Db 113 -----REFSLILITCGTILSGPF--ALANWLYSGM---BEYTYITRSVVFILS 156  
 QY 172 -----QVVFVAILLHSHLECREPILIPILSLVWGAALVRCTTLCGYKXNHHI 218



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Db 157 LILFLVLRPEDYVFASISLFSLSN-----ILNLWHSR-----HFINI-- 198
Qy 219 IIPDRSGPLGDATIRKMLSF-----WWPLALILATORISRPVNLVFSRD--LGGS 269
Db 199 -----KLYKNLOFKYHFKPMWYLFASLLA-----VNIYTNLDTVMLG 236
Qy 270 SAATEAVAILTATYVGHMPYGMWTEIRAV-YPA-----FDKNPNPN--KLIVSTNTVTAA 322
Db 237 INGEAVGYVSVASKVWILLSLITSISAVLLRLSFYISKNDTSNFKMLKESSAV--- 293
Qy 323 HIKKFTFCVMSLTLFCFWFWNTVNSEKILIDIGVDFAFALC---VVPLRIFSPFPV 379
Db 294 -----IFFTAIPL-----WVFFIVEAKDSILL-LGGSQYLPATLAMQILMILLISGF-- 340
Qy 380 PVTVAHLTG-----WMLTKKTFVLAPSSVLRIRIIVLIASLVVLYLGVHGATLGVGSLLA 435
Db 341 -----SNITGNQILIPMNRKYFMVA-VTIGAVINLIILMLLMPKFGIIGAS--VATLFA 392

RESULT 14
Q07870 ID C07870 PRELIMINARY; PRT; 481 AA.
AC C07870;
DT 01-JUL-1997 (TremBLrel. 04, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DE Putative oligosaccharide repeat unit transporter.
GN CPS19BU.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97386440; PubMed=9244289;
RA Morona J.K., Morona R., Paton J.C.;
RT "Molecular and genetic characterization of the capsule biosynthesis
RT locus of Streptococcus pneumoniae type 19B.";
RL J. Bacteriol. 179:4953-4958 (1997).
DR EMBL; AF064325; AAB66524.1;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; P:Polysacc synt.
DR Pfam; PF01943; Polyseacc synt; 1.
SQ SEQUENCE 481 AA; 53853 MW; C09A07D7D1AB5FD6 CRC64;

Query Match 4.6%; Score 117; DB 2; Length 481;
Best Local Similarity 21.0%; Pred. No. 0.19;
Matches 101; Conservative 85; Mismatches 136; Indels 158; Gaps 29;

Qy 4 FPALTYWPLI-RFLVP--LGITNTAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMK 60
Db 23 PFLIT--FPYISRIILNPNGILGTSFFSIG-----NYGI-----LLASLGI----- 61
Qy 61 FTGPMSPFNKVLVFNVSCKDRTKAVL--CMVAGATAAVPHLTIAYSDLYGIYINKLH 118
Db 62 -----STYGIKAVASVDRDRDKLSKVQCELMINAVSIITAILLFMTI---FITOLN 112
Qy 119 HYDESVGSKTRAFIYL-----AAPPFMDAMWATHAGILLKKKYSFLVGCASISDVIA 171
Db 113 -----REFSLLITCGTILSSPF--ALNWLYSGM--BEYVITTRS VVVFKLS 156
Qy 172 -----QVVFVAILHSHLECBELIIPILSYMGALVRCCTLCGYKNIHD 218
Db 157 LILFLVLRPEDYVFASISLFSLSN-----ILNLWHSR-----HFINI-- 198
Qy 219 IIPDRSGPLGDATIRKMLSF-----WWPLALILATORISRPVNLVFSRD--LGGS 269
Db 199 -----KLYKNLOFKYHFKPMWYLFASLLA-----VNIYTNLDTVMLG 236
Qy 270 SAATEAVAILTATYVGHMPYGMWTEIRAVPA-----FDKNPNPN--KLIVSTNTVTAA 322

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Db 237 INGEAVGYVSVASKVWILLSLITSISAVLLRLSFYISKNDTSNFKMLKESSAV--- 293
Qy 323 HIKKFTFCVMSLTLFCFWFWNTVNSEKILIDIGVDFAFALC---VVPLRIFSPFPV 379
Db 294 -----IFFTAIPL-----WVFFIVEAKDSILL-LGGSQYLPATLAMQILMILLISGF-- 340
Qy 380 PVTVAHLTG-----WMLTKKTFVLAPSSVLRIRIIVLIASLVVLYLGVHGATLGVGSLLA 435
Db 341 -----SNITGNQILIPMNRKYFMVA-VTIGAVINLIILMLLMPKFGIIGAS--VATLFA 392

RESULT 15
Q09104 ID Q09104 PRELIMINARY; PRT; 535 AA.
AC Q09104;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE 4F21c-5.
DE 4F21c-5.
GN Oryctolagus cuniculus (Rabbit).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20473842; PubMed=10631289;
RA Rajan D.P., Kekuda R., Huang W., Devoe L.D., Leibach F.H.,
RA Prasad P.D., Ganapathy V.;
RT "Cloning and functional characterization of a Na(+)-independent,
RT broad-specific neutral amino acid transporter from mammalian
RT intestine.";
RL Biochim. Biophys. Acta 1463:6-14 (2000).
DR EMBL; AF170106; AAF26282.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015359; F:amino acid permease activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel permeasel.
DR InterPro; IPR004760; LAA transporter.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; aa permeases; 1.
DR TIGRFAMs; TIGR00911; 2A0308; 1.
SQ SEQUENCE 535 AA; 58321 MW; D4939C0F971CB190 CRC64;

Query Match 4.6%; Score 117; DB 6; Length 535;
Best Local Similarity 21.8%; Pred. No. 0.21;
Matches 120; Conservative 73; Mismatches 201; Indels 156; Gaps 30;

Qy 28 DRGEQALNRGIAAVKEDAVEMLASYGLAYSLM---KFTGPMSPFNKVLVFNVSCKDR 84
Db 23 DPPEASSGGGVALKKE-IGLVSACTIVGNITIGSGIFVSPKGVLENAGSVGL----- 74
Qy 85 KAVLCMVVAGATAAVPHLTIAYSDLYGIYINKLHHVDES VG--SKTRAFIYLAAPPFMD 142
Db 75 -AVIVWIVTGLTAV--GALCYAELGVTI-----PKSGGDYVYKDFGGLAGF---- 120
Qy 143 AMWATHAGILLKKKYSFLVGCASISDVIAQVVF-----VAILLHSHLECR 187
Db 121 LRLW--IAVLVITYPTNQAVIALTFSNYLQPLFPTCFPPDSGLRLAALCLLLTWNGS 178
Qy 188 E-----PLLIPILSLYMGALVRCCTLCGYI-----KNIHDIIPDRSGPEL 228
Db 179 SVRWATRVQDIFTAGKLLALALIINGVV---QICKGEYFWLEPCVAFNQE---PDI 231
Qy 229 GGDATIRKMLSF---WWPLALILATORISRPVNL-----FVSRDLGGSSAATEAVAILTA 281
Db 232 GLIALAFLOGSPAYGGWNF-LNYVTEELVDYKPLPRAIFISIPLVTFYVVFANVAYITA 290
Qy 282 TVP-----VGHMPYGMWTEIRAVVPAFDKNPNKNKLVST----- 316
Db 291 MSPQELLASNAVATPGEKILGVM--AWIMPISVALSTFGVNGS--LETSSRLPFAGAR 346

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Db 1801 CATAACCCCTGCTCAAGAAACCCAAAGACACAGCTGCTCAGCGTTACAGCTTGTGTC 1860  
Qy 1861 TCCTCCCTGGAACAATCTCTCTTGAACCAAGGACTCAGCTGTGCATCGCCCTCG 1920  
Db 1861 TCCTCCCTGGAACAATCTCTCTTGAACCAAGGACTCAGCTGTGCATCGCCCTCG 1920  
Qy 1921 GTACCCCTGACAGAGGACACAGCTCTCTGCTCCCTTCTATCTCTTAAAGATCA 1980  
Db 1921 GTACCCCTGACAGAGGACACAGCTCTCTGCTCCCTTCTATCTCTTAAAGATCA 1980  
Qy 1981 CAGTTTAAACTCGGCTCTCTTGAATTTGCTTCCAGTCCATGCGCTACAAAGATG 2040  
Db 1981 CAGTTTAAACTCGGCTCTCTTGAATTTGCTTCCAGTCCATGCGCTACAAAGATG 2040  
Qy 2041 GAGCCCGGTGGCTCTTAAATTTCCCTTCTGCGAGGATTCACATGCGCTACAAAGATG 2100  
Db 2041 GAGCCCGGTGGCTCTTAAATTTCCCTTCTGCGAGGATTCACATGCGCTACAAAGATG 2100  
Qy 2101 ACATGAGGAGGCGGTGGCAAGTTCAGATGCGAGTCCCGTTCACATGAGAAACGGA 2160  
Db 2101 ACATGAGGAGGCGGTGGCAAGTTCAGATGCGAGTCCCGTTCACATGAGAAACGGA 2160  
Qy 2161 GACCTGTGACACAGAGGCTGACAGATGAGACAGATCTCCGTTAGAAAGTTTGGTTG 2220  
Db 2161 GACCTGTGACACAGAGGCTGACAGATGAGACAGATCTCCGTTAGAAAGTTTGGTTG 2220  
Qy 2221 AAATGCCCCGGGCGGACCAACTGACATGTTGATGATAGCATTTTCACTCTCGTTCTC 2280  
Db 2221 AAATGCCCCGGGCGGACCAACTGACATGTTGATGATAGCATTTTCACTCTCGTTCTC 2280  
Qy 2281 CTAGATCTGACAAAGCTGTAGTTCTCACCCCCCGTGTATATATACATGAGCTAACTTT 2340  
Db 2281 CTAGATCTGACAAAGCTGTAGTTCTCACCCCCCGTGTATATATACATGAGCTAACTTT 2340  
Qy 2341 TTAATTTGTCACAAAGGCGATCTCCAGATGCGAGCTTCCGCTGATGCTTTTCCCTGAA 2400  
Db 2341 TTAATTTGTCACAAAGGCGATCTCCAGATGCGAGCTTCCGCTGATGCTTTTCCCTGAA 2400  
Qy 2401 GCTTGTCTTTTCCCTGCTGCTTCTTGAAGTTCGATGAGCGAGTCAATGAGCATCC 2460  
Db 2401 GCTTGTCTTTTCCCTGCTGCTTCTTGAAGTTCGATGAGCGAGTCAATGAGCATCC 2460  
Qy 2461 TAACTTTGCTTTTACAGTGAATGAGCTTTTACAGTGAATGAGCTTTTACAGTGAATGAGCTTTT 2520  
Db 2461 TAACTTTGCTTTTACAGTGAATGAGCTTTTACAGTGAATGAGCTTTTACAGTGAATGAGCTTTT 2520  
Qy 2521 TGCCAGGTTGCTGAGGTAATTTTGAAGTAGATATATATACCTGGTTCTGCTATCCTTA 2580  
Db 2521 TGCCAGGTTGCTGAGGTAATTTTGAAGTAGATATATATACCTGGTTCTGCTATCCTTA 2580  
Qy 2581 GTCCATACTCTCGGTACAGGTAATGAGATGAGTACTAGCTTCCCTCCACACCAT 2640  
Db 2581 GTCCATACTCTCGGTACAGGTAATGAGATGAGTACTAGCTTCCCTCCACACCAT 2640  
Qy 2641 AGGATAAGCAAGACATTTTAAAGATACAGAGTCACTATGTTGCTTCCCTCCCTGAATA 2700  
Db 2641 AGGATAAGCAAGACATTTTAAAGATACAGAGTCACTATGTTGCTTCCCTCCCTGAATA 2700  
Qy 2701 AGGATTCGAATTCATGAGTGAATTTTCTAGTTTGGAAAGCAGGTTTCTT 2760  
Db 2701 AGGATTCGAATTCATGAGTGAATTTTCTAGTTTGGAAAGCAGGTTTCTT 2760  
Qy 2761 CTTTAAAGAAATTTAGACACAGGTTTCACTAAATTTAGTTAGTCAAGATTTCTAGACTGA 2820  
Db 2761 CTTTAAAGAAATTTAGACACAGGTTTCACTAAATTTAGTTAGTCAAGATTTCTAGACTGA 2820  
Qy 2821 AAGAACTTAAACCAAAATATTTTAAAGATATATATATCTCTGTATATGTTATGTAAT 2880  
Db 2821 AAGAACTTAAACCAAAATATTTTAAAGATATATATATCTCTGTATATGTTATGTAAT 2880  
Qy 2881 TTAATTTAGCTATATACATTTCTTATTTTCCGATTTTCAATAAAATGCTCTCTAATACA 2940  
Db 2881 TTAATTTAGCTATATATACATTTCTTATTTTCCGATTTTCAATAAAATGCTCTCTAATACA 2940

Qy 2941 AAAAA 2945  
Db 2941 AAAAA 2945  
RESULT 2  
US-09-978-697-6  
; Sequence 6, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: F2630PIC27  
; CURRENT APPLICATION NUMBER: US/09/978,697  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918595  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
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; PRIOR FILING DATE: 1998-03-10  
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Query Match 100.0%; Score 2945; DB 9; Length 2945;
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APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuc, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C83  
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CURRENT FILING DATE: 2001-10-24  
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PRIOR FILING DATE: 2001-07-30  
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Qy 181 CTTGACCGGGGCAATGCTGCTCAAGGAGGATGAGTCAGATGCTGCCAGCTACGG 240
Db 181 CTTGACCGGGGCAATGCTGCTCAAGGAGGATGAGTCAGATGCTGCCAGCTACGG 240
Qy 241 GCTGGCGTACTCCCTCATGAAGTTCTTACGGGTCCCATGAGTGACTTCAAAATGTGG 300
Db 241 GCTGGCGTACTCCCTCATGAAGTTCTTACGGGTCCCATGAGTGACTTCAAAATGTGG 300
Qy 301 CCTGGTGTGTTGTAACAGCAAGAGAGACAGGACCAAGCCCTCTCTGTATGTGTGGC 360
Db 301 CCTGGTGTGTTGTAACAGCAAGAGAGACAGGACCAAGCCCTCTCTGTATGTGTGGC 360
Qy 361 AGGGGCGATCGCTGCCGTCTTTCACACTGATAGCTTATAGTGAATTTAGGATPACTAT 420
Db 361 AGGGGCGATCGCTGCCGTCTTTCACACTGATAGCTTATAGTGAATTTAGGATPACTAT 420
Qy 421 TATCAATAAATGCAATGTCAGCGAGTGGGAGGAGCAAGAGGAGGAGGAGGAGGAGGAGG 480
Db 421 TATCAATAAATGCAATGTCAGCGAGTGGGAGGAGCAAGAGGAGGAGGAGGAGGAGGAGG 480
Qy 481 GTACCTCGCGCCCTTCTTTCATGAGCAATGAGTGGATGAGTGGATGAGTGGATGAGTGGAT 540
Db 481 GTACCTCGCGCCCTTCTTTCATGAGCAATGAGTGGATGAGTGGATGAGTGGATGAGTGGAT 540
Qy 541 AAAACACAAATACAGTTTCTGCTGGATGAGTGGATGAGTGGATGAGTGGATGAGTGGATGAGT 600
Db 541 AAAACACAAATACAGTTTCTGCTGGATGAGTGGATGAGTGGATGAGTGGATGAGTGGATGAGT 600
Qy 601 TGTGTTGTAGCCATTTGCTTCAAGTCACTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 601 TGTGTTGTAGCCATTTGCTTCAAGTCACTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Qy 661 GATCCTCTCTGTTGATAGTGGGCGACTTGTGCGCTGCAACCCCTGTGCTGGGCTACTA 720
Db 661 GATCCTCTCTGTTGATAGTGGGCGACTTGTGCGCTGCAACCCCTGTGCTGGGCTACTA 720
Qy 721 CAAGAACATTCAGACATCATCTGACAGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGG 780
Db 721 CAAGAACATTCAGACATCATCTGACAGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGG 780
Qy 781 AATAAGAAAGATGCTGAGCTTGTGGGCTTTGGGCTTAAATTTGCGGCAACAGAGAAAT 840
Db 781 AATAAGAAAGATGCTGAGCTTGTGGGCTTTGGGCTTAAATTTGCGGCAACAGAGAAAT 840
Qy 841 CAGTCGGCCTATTGTCACACCTCTTTGTTCCCGGAGCTTGGTGGAGTGGTGGAGTGGTGGAGTGG 900
Db 841 CAGTCGGCCTATTGTCACACCTCTTTGTTCCCGGAGCTTGGTGGAGTGGTGGAGTGGTGGAGTGG 900
Qy 901 AGAGGAGTGGCGATTTTGAAGCCACATACCTGTGGGTCAATGCGCATACGGCTGGTT 960
Db 901 AGAGGAGTGGCGATTTTGAAGCCACATACCTGTGGGTCAATGCGCATACGGCTGGTT 960
Qy 961 GACGGAATCGTGTGTGTATCTGCTTTGAGAGAGATTAACCCAGCAGCAAACTGGT 1020
Db 961 GACGGAATCGTGTGTGTATCTGCTTTGAGAGAGATTAACCCAGCAGCAAACTGGT 1020
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Db 961 GACGGAAATCGTGTGTATCTCTGTTTCGACAGAAATAACCCAGCAACAACTGGT 1020  
Qy 1021 GAGCAGGAGCAACACAGTCAGGAGCCCAACATCAAGAAAGTTACCTTCCTCTGCATGGC 1080  
Db 1021 GAGCAGGAGCAACACAGTCAGGAGCCCAACATCAAGAAAGTTACCTTCCTCTGCATGGC 1080  
Qy 1081 TCTGTCACTACGCT 1140  
Db 1081 TCTGTCACTACGCT 1140  
Qy 1141 GATAGACATCATCGGAGTGGACTTTCCTTTTGAGAACTCTGTGTCTCTCTCTCTCTCTCT 1200  
Db 1141 GATAGACATCATCGGAGTGGACTTTCCTTTTGAGAACTCTGTGTCTCTCTCTCTCTCTCT 1200  
Qy 1201 CT 1260  
Db 1201 CT 1260  
Qy 1261 ACTGAAGAAACCTTCCT 1320  
Db 1261 ACTGAAGAAACCTTCCT 1320  
Qy 1321 CAGCCT 1380  
Db 1321 CAGCCT 1380  
Qy 1381 CTTGCGGCGCTTGTGGAGAAATCCACATGGTGGCGCATCTGTGTCGGGATCATCTCTCTCT 1440  
Db 1381 CTTGCGGCGCTTGTGGAGAAATCCACATGGTGGCGCATCTGTGTCGGGATCATCTCTCTCT 1440  
Qy 1441 GAAACAGAAAGAAAGATGGAGATGAGTGGCGGACAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Db 1441 GAAACAGAAAGAAAGATGGAGATGAGTGGCGGACAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Qy 1501 AGACATGCTCGGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGGAGGAGGAGGAG 1560  
Db 1501 AGACATGCTCGGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGGAGGAGGAGGAG 1560  
Qy 1561 AGGACGCGGAGCGCATGGGAGTCTGAGGAGGAGTCTGAGGAGGAGTCTGAGGAGGAGTCT 1620  
Db 1561 AGGACGCGGAGCGCATGGGAGTCTGAGGAGGAGTCTGAGGAGGAGTCTGAGGAGGAGTCT 1620  
Qy 1621 CT 1680  
Db 1621 CT 1680  
Qy 1681 GGCCTTGATTTAAAGTTTCGTGCAATCTCTAGCATCTGGGTATGCTCAGCTGACG 1740  
Db 1681 GGCCTTGATTTAAAGTTTCGTGCAATCTCTAGCATCTGGGTATGCTCAGCTGACG 1740  
Qy 1741 GGGGACCTAGTGAATGCTCTTTACTGTGTCTATGTATGTAATAAACAACGAACTGACTT 1800  
Db 1741 GGGGACCTAGTGAATGCTCTTTACTGTGTCTATGTATGTAATAAACAACGAACTGACTT 1800  
Qy 1801 CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCAGGTTGAGCTGTGCTCC 1860  
Db 1801 CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCAGGTTGAGCTGTGCTCC 1860  
Qy 1861 TCCTCCCTGAGCAATCT 1920  
Db 1861 TCCTCCCTGAGCAATCT 1920  
Qy 1921 GTCACCCCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980  
Db 1921 GTCACCCCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980  
Qy 1981 CAGGTTAAACCTCGGCTTCT 2040  
Db 1981 CAGGTTAAACCTCGGCTTCT 2040  
Qy 2041 GAGCCCCGGTGGCTCTTAAATTTCCCTTCTGCAAGGAGTTCGAAACCATCTACTCCAC 2100  
Db 2041 GAGCCCCGGTGGCTCTTAAATTTCCCTTCTGCAAGGAGTTCGAAACCATCTACTCCAC 2100

## RESULT 5

US-09-978-189-6

; Sequence 6, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

Qy 2101 ACATCAGAGGCGGTCGCGACGTCGACCGCGGAGTCCCGTTCCACTCAGGAACGGA 2160  
Db 2101 ACATCAGAGGCGGTCGCGACGTCGACCGCGGAGTCCCGTTCCACTCAGGAACGGA 2160  
Qy 2161 GACCTGTGACCAACAGCAGGCTGACAGATGAGAGAAATCTCCCGTAGAAAGGTTGGTTG 2220  
Db 2161 GACCTGTGACCAACAGCAGGCTGACAGATGAGAGAAATCTCCCGTAGAAAGGTTGGTTG 2220  
Qy 2221 AAATCCCGGGGCGAGCAAACTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
Db 2221 AAATCCCGGGGCGAGCAAACTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
Qy 2281 CTAGATCTGAGCAAGCTGTGACGTTCTCAGTTCACCCCGACCGTGTATATACATGAGTAACCTTT 2340  
Db 2281 CTAGATCTGAGCAAGCTGTGACGTTCTCAGTTCACCCCGACCGTGTATATACATGAGTAACCTTT 2340  
Qy 2341 TTAATTTGTCACAAAGCGCATCTCCAGATTCAGACCCCTGCCGATGACATTTTCTCTGAA 2400  
Db 2341 TTAATTTGTCACAAAGCGCATCTCCAGATTCAGACCCCTGCCGATGACATTTTCTCTGAA 2400  
Qy 2401 GGCCTTGCCTTTCCCTCGCTTTCTCTGAAGTGGCATTAGAGCGAGTCAATGGAGCATCC 2460  
Db 2401 GGCCTTGCCTTTCCCTCGCTTTCTCTGAAGTGGCATTAGAGCGAGTCAATGGAGCATCC 2460  
Qy 2461 TTAATTTGCAATTTAGTTTACAGTGAACCTGAGCTTTAAGTCTCATCCAGCATCTAA 2520  
Db 2461 TTAATTTGCAATTTAGTTTACAGTGAACCTGAGCTTTAAGTCTCATCCAGCATCTAA 2520  
Qy 2521 TGCAGGTTGCTGTAGGTTAACTTTTGAAGTAGATATATTTACCTGGTCTGTCTCTTAA 2580  
Db 2521 TGCAGGTTGCTGTAGGTTAACTTTTGAAGTAGATATATTTACCTGGTCTGTCTCTTAA 2580  
Qy 2581 GTCATAACTCTCGGTCAGGTAATGAGAAATGTAAGTACTACGGTACTTCCCTCCCAACCAT 2640  
Db 2581 GTCATAACTCTCGGTCAGGTAATGAGAAATGTAAGTACTACGGTACTTCCCTCCCAACCAT 2640  
Qy 2641 AGGATAAAGCAAGACATTTTATAAGCATACAGAGTCACTATGCTGCTCTCCCTGAAATA 2700  
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Qy 2701 AGCATTCGAAATCCATGCGAGTCACTATTTTCTAAGTTTGGAAAGCAGGTTTCTT 2760  
Db 2701 AGCATTCGAAATCCATGCGAGTCACTATTTTCTAAGTTTGGAAAGCAGGTTTCTT 2760  
Qy 2761 CTTTAAAGAAATTAAGACAGGTTCACTAAATGATTAGTCAGAAATCTCTAGACTGA 2820  
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Qy 2821 AAGAACCTTAAACAAAAAATATTTTAAAGATATAATATATGCTGTATATGTTATGTAAT 2880  
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Qy 2881 TTATTTTAGGCTTAATACATTTCTCTATTTTCCGATTTTCAATAAATGCTCTTAATACA 2940  
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Qy 2941 AAAAA 2945  
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## RESULT 5

US-09-978-189-6

; Sequence 6, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C7  
CURRENT APPLICATION NUMBER: US/09/978,189  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/085311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
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; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
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; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGTCGCCCGCTCGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60
DB      1  CGCTGCCCGCTCGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60

QY      61  GGGTCAGCCACCGCGGGGACTATGGTGAATTCGCCGGGCTCAGCAGCTACTGGCCCT 120
DB      61  GGGTCAGCCACCGCGGGGACTATGGTGAATTCGCCGGGCTCAGCAGCTACTGGCCCT 120

QY      121  GATCCGGTCTTGTGTCCTTGGGATCACCACATAGCATCGACTTCGGGGAGCAGGC 180
DB      121  GATCCGGTCTTGTGTCCTTGGGATCACCACATAGCATCGACTTCGGGGAGCAGGC 180

QY      181  CTTGAACCGGGGCAATGCTGCTCAAGGAGGATCAGTCGAGATGCTGGCCAGTACGG 240
DB      181  CTTGAACCGGGGCAATGCTGCTCAAGGAGGATCAGTCGAGATGCTGGCCAGTACGG 240

QY      241  GCTGGGCTACTCCCTCATGAGTCTTACGGGTCCCATGAGTGAATTCAGAAATGTGG 300
DB      241  GCTGGGCTACTCCCTCATGAGTCTTACGGGTCCCATGAGTGAATTCAGAAATGTGG 300

QY      301  CTTGGTGTGTTGTGAACAGCAAGAGACAGAGCCAAAGCCGCTCCTGTGTATGGTGTGC 360
DB      301  CTTGGTGTGTTGTGAACAGCAAGAGACAGAGCCAAAGCCGCTCCTGTGTATGGTGTGC 360

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361  AGGGGCCATCGCTCGCTCTTTTACACACTGATAGCTTATAGTGAATTTAGGATACTACAT 420
DB      AGGGGCCATCGCTCGCTCTTTTACACACTGATAGCTTATAGTGAATTTAGGATACTACAT 420

421  TATCAATAAATGCAACATGTGGAGAGTGGTGGGAGCAAGACGAGAGAGCCCTTCT 480
DB      TATCAATAAATGCAACATGTGGAGAGTGGTGGGAGCAAGACGAGAGAGCCCTTCT 480

481  GTACCTCGCGGCTTCTTCTTCATGAGCAATGCGATGGACCCCATGCTGGCAATCTCT 540
DB      GTACCTCGCGGCTTCTTCTTCATGAGCAATGCGATGGACCCCATGCTGGCAATCTCT 540

541  AAAACACAATAACAGTTCCTGGTGGATGTGCCCTCAATCTCAGATGTCATAGCTCAGGT 600
DB      AAAACACAATAACAGTTCCTGGTGGATGTGCCCTCAATCTCAGATGTCATAGCTCAGGT 600

601  TGTCTTTGTAGCCATTTTGTCTTACAGTCACTGGAATGCCGGAGCCCTGCTCATCCC 660
DB      TGTCTTTGTAGCCATTTTGTCTTACAGTCACTGGAATGCCGGAGCCCTGCTCATCCC 660

661  GATCCTCTCTTGTATACATGGGCGCACTTGTGGCTGSCACACCCCTGTGCTGGGTACTA 720
DB      GATCCTCTCTTGTATACATGGGCGCACTTGTGGCTGSCACACCCCTGTGCTGGGTACTA 720

721  CAAGAACATTCAGACATCATCTCTGACAGAGTGGCCGGAGCTGGGGGAGATGCAAC 780
DB      CAAGAACATTCAGACATCATCTCTGACAGAGTGGCCGGAGCTGGGGGAGATGCAAC 780

781  AATAAGAAAGATGCTGAGCTTCTGTGGCTTTTGGCTCTAATTTCTGGCCACACAGAGAT 840
DB      AATAAGAAAGATGCTGAGCTTCTGTGGCTTTTGGCTCTAATTTCTGGCCACACAGAGAT 840

841  CAGTGGCCCTATGTGCAACTCTTTTCCCGGAGCCTTGGTGGAGTCTGGCAGTCTGCAAGCCAC 900
DB      CAGTGGCCCTATGTGCAACTCTTTTCCCGGAGCCTTGGTGGAGTCTGGCAGTCTGCAAGCCAC 900

901  AGAGGCAGTGGCGATTTTGCACAGCCACATACCTTGTGGTGCACATGCCATACGGTGGT 960
DB      AGAGGCAGTGGCGATTTTGCACAGCCACATACCTTGTGGTGCACATGCCATACGGTGGT 960

961  GACGAAATCCGTGTGTGTCTGCTTTCAGAAAGATTAACCCAGCAACAAATGCT 1020
DB      GACGAAATCCGTGTGTGTCTGCTTTCAGAAAGATTAACCCAGCAACAAATGCT 1020

1021  GAGCAGAGCAACACAGTCAAGCCACACATCAAGAAAGTTCACCTTCTGTCATGCG 1080
DB      GAGCAGAGCAACACAGTCAAGCCACACATCAAGAAAGTTCACCTTCTGTCATGCG 1080

1081  TCTGTCACTACGCTCTGTTTGTGTGATTTTGGACACCCACGTCGTGAGAAATCTT 1140
DB      TCTGTCACTACGCTCTGTTTGTGTGATTTTGGACACCCACGTCGTGAGAAATCTT 1140

1141  GATAGACATCATCGGAGTGGACTTTGCTTTGAGAACTCTGTTGTTGTTCTTTGGGGAT 1200
DB      GATAGACATCATCGGAGTGGACTTTGCTTTGAGAACTCTGTTGTTGTTCTTTGGGGAT 1200

1201  CTTCTCCTTCTCCAGTTCAGTCAAGTGGGCGCATCTCACCGGTGGGTGATGAC 1260
DB      CTTCTCCTTCTCCAGTTCAGTCAAGTGGGCGCATCTCACCGGTGGGTGATGAC 1260

1261  ACTGAAGAAACCTTCTGCTTCCCGCAGCTGCTGTCGGGATCATGTCCTCATCGC 1320
DB      ACTGAAGAAACCTTCTGCTTCCCGCAGCTGCTGTCGGGATCATGTCCTCATCGC 1320

1321  CAGCCTCGTGGTCTTACCTTACCTGGGGGTGCAAGTGGGACCTTGGGGTGGGCTCCCT 1380
DB      CAGCCTCGTGGTCTTACCTTACCTGGGGGTGCAAGTGGGACCTTGGGGTGGGCTCCCT 1380

1381  CTTGGCGGCTTGTGGGAGATCCACCATGCTGGCCATGCTGCTGCTATGCTACCG 1440
DB      CTTGGCGGCTTGTGGGAGATCCACCATGCTGGCCATGCTGCTGCTATGCTACCG 1440

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QY 2701 AGCATTCGAATCCATGCGAGTGCAGTATATATTTTCTAAGTTTTCGAAAGCAGGTTTTT 2760  
Db 2701 AGCATTCGAATCCATGCGAGTGCAGTATATATTTTCTAAGTTTTCGAAAGCAGGTTTTT 2760  
QY 2761 CTTTAAAAAATTATAGACAGGTTTCACTAAATGATTAGTACAGATTCCTAGACTGA 2820  
Db 2761 CTTTAAAAAATTATAGACAGGTTTCACTAAATGATTAGTACAGATTCCTAGACTGA 2820  
QY 2821 AAGAACCTAAACAAAAAATATTTTAAAGATATAAATATATCTGTATATGTATGTAAT 2880  
Db 2821 AAGAACCTAAACAAAAAATATTTTAAAGATATAAATATATCTGTATATGTATGTAAT 2880  
QY 2881 TTATTTAGCTATATACATTTCTCTATTTTCCATTTTCAATAAAATGCTCTCTAATACA 2940  
Db 2881 TTATTTAGCTATATACATTTCTCTATTTTCCATTTTCAATAAAATGCTCTCTAATACA 2940  
QY 2941 AAAAA 2945  
Db 2941 AAAAA 2945

RESULT 8

US-09-978-191A-6  
; Sequence 6, Application US/09978191A  
; Publication No. US20030050239A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830FIC4  
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Db 61 GGGTCAGCCACAGCGGGGGGACTATGTTGAAATTCGCCGCTCAGCAGTACTGCCCT 120  
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: GENERAL INFORMATION:  
: APPLICANT: Ashkenazi, Avi  
: APPLICANT: Baker Kevin P.  
: APPLICANT: Borstein, David  
: APPLICANT: Desnoyers, Luc



APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.  
APPLICANT: Kuo, Sophia S.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C17  
CURRENT APPLICATION NUMBER: US/09/978.403A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
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Qy 241 GCTGGCGTACTCCCTCATGAAGTCTTTCACGGGTCCCATGAGTACTTCAAAAATGTGG 300  
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Db 301 CTTGGTGTGTTGACAGCAGAGAGACAGGACCAAGCCGTCCTGTGTATGTGGTGGC 360

Qy 361 AGGGGCCATCGCTGCGCTCTTTCACACACTGATAGTATATAGTATTTAGGATACAT 420  
Db 361 AGGGGCCATCGCTGCGCTCTTTCACACACTGATAGTATATAGTATTTAGGATACAT 420

Qy 421 TATCAATAAAGTCCACCATGTGACGAGTGGTGGGACGACGAGAGAGGGCCCTTCT 480  
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Qy 481 GTACCTCGCGCCCTTTCCTTTTCATGACCAATGCGATGAGACCCCATGCTGCAATCTCT 540  
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Qy 541 AAAACAAATACAGTTTCTGTGGGATGTGCTCAATCTCAGATGATAGCTCAGGT 600  
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Qy 601 TGTGTTGTAGCCATTTGCTTTCACAGTCACTGGAATGCCGGAGCCCTGCTCATCCC 660  
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; Publication No. US20030054405A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
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; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630F1C65  
; CURRENT APPLICATION NUMBER: US/09/999,833A  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25



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RESULT 12

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; Sequence 6, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara Napoleon  
; APPLICANT: Flvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuc, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC12  
; CURRENT APPLICATION NUMBER: US/09/981,915A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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RESULT 13
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; Sequence 6, Application US/09978824
; Publication NO. US20030055216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deeneyers, Luc
; APPLICANT: Saton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Nepier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/085697

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## RESULT 14

US-09-918-585A-6  
; Sequence 6, Application US/09918585A  
; Publication No. US20030060406A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
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APPLICANT: Tumas, Daniel  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PICI  
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PRIOR APPLICATION NUMBER: 60/083495  
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PRIOR APPLICATION NUMBER: 60/083496  
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PRIOR APPLICATION NUMBER: 60/083559  
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PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
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## RESULT 15

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APPLICANT: Botstein, David

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APPLICANT: Gerber, Hanspeter

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APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

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APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

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APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2630P121

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1	PRIOR FILING DATE: 1998-04-15
2	PRIOR APPLICATION NUMBER: 60/081819
3	PRIOR FILING DATE: 1998-04-15
4	PRIOR APPLICATION NUMBER: 60/081952
5	PRIOR FILING DATE: 1998-04-15
6	PRIOR APPLICATION NUMBER: 60/081838
7	PRIOR FILING DATE: 1998-04-15
8	PRIOR APPLICATION NUMBER: 60/082568
9	PRIOR FILING DATE: 1998-04-21
10	PRIOR APPLICATION NUMBER: 60/082569
11	PRIOR FILING DATE: 1998-04-21
12	PRIOR APPLICATION NUMBER: 60/082704
13	PRIOR FILING DATE: 1998-04-22
14	PRIOR APPLICATION NUMBER: 60/082804
15	PRIOR FILING DATE: 1998-04-22
16	PRIOR APPLICATION NUMBER: 60/082700
17	PRIOR FILING DATE: 1998-04-22
18	PRIOR APPLICATION NUMBER: 60/082797
19	PRIOR FILING DATE: 1998-04-22
20	PRIOR APPLICATION NUMBER: 60/082796
21	PRIOR FILING DATE: 1998-04-23
22	PRIOR APPLICATION NUMBER: 60/083336
23	PRIOR FILING DATE: 1998-04-27
24	PRIOR APPLICATION NUMBER: 60/083322
25	PRIOR FILING DATE: 1998-04-28
26	PRIOR APPLICATION NUMBER: 60/083392
27	PRIOR FILING DATE: 1998-04-29
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37	PRIOR FILING DATE: 1998-04-29
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39	PRIOR FILING DATE: 1998-04-29
40	PRIOR APPLICATION NUMBER: 60/083559
41	PRIOR FILING DATE: 1998-04-29
42	PRIOR APPLICATION NUMBER: 60/083500
43	PRIOR FILING DATE: 1998-04-29
44	PRIOR APPLICATION NUMBER: 60/083742
45	PRIOR FILING DATE: 1998-04-30
46	PRIOR APPLICATION NUMBER: 60/084366
47	PRIOR FILING DATE: 1998-05-05
48	PRIOR APPLICATION NUMBER: 60/084414
49	PRIOR FILING DATE: 1998-05-06
50	PRIOR APPLICATION NUMBER: 60/084441
51	PRIOR FILING DATE: 1998-05-06
52	PRIOR APPLICATION NUMBER: 60/084637
53	PRIOR FILING DATE: 1998-05-07
54	PRIOR APPLICATION NUMBER: 60/084639
55	PRIOR FILING DATE: 1998-05-07
56	PRIOR APPLICATION NUMBER: 60/084627
57	PRIOR FILING DATE: 1998-05-07
58	PRIOR APPLICATION NUMBER: 60/084643
59	PRIOR FILING DATE: 1998-05-07
60	PRIOR APPLICATION NUMBER: 60/085339
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62	PRIOR APPLICATION NUMBER: 60/085338
63	PRIOR FILING DATE: 1998-05-13
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65	PRIOR FILING DATE: 1998-05-13
66	PRIOR APPLICATION NUMBER: 60/085582
67	PRIOR FILING DATE: 1998-05-15

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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      100.0%; Score 2945; DB 10; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GGGTACGCCACGGCGGAGATGTGTGAAATCCGGGCGTACGCACTACTGGCCCT 120

Qy 121 GATCGGTTCTTGGTCCCTCGGCGATCACCAATAGCCATCGACTTCGGGGAGCAGGC 180
Db 121 GATCGGTTCTTGGTCCCTCGGCGATCACCAATAGCCATCGACTTCGGGGAGCAGGC 180

Qy 181 CTTGAACCGGGCAATGTGTGTCAAGAGATGCAAGATGTCAGTGTGGCCAGCTACGG 240
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Qy 241 GGTGGCTACTCCCTCATGAGTCTTCAACGGTCCCATGAGTACCTCAAAAATGTGG 300
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Qy 361 AGGGCCATCGTGGGCTTTTCAACACTGATGATCTTATAGTATTTAGGATACTACAT 420
Db 361 AGGGCCATCGTGGGCTTTTCAACACTGATGATCTTATAGTATTTAGGATACTACAT 420

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Qy 721 CAAGAACATTCAGACATCATCCCTGACAGAGTGGCCGAGCTGGGGGAGATGCAAC 780
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Qy 781 AATAAGAGATGCTGGGCTTCTGTGGCTTTGGCTTAAATCTGGCCACACAGAGAT 840
Db 781 AATAAGAGATGCTGGGCTTCTGTGGCTTTGGCTTAAATCTGGCCACACAGAGAT 840

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Db	2881	TTATTTTAGGCTATATACATTTTCTATTTTCGCATTTTCAATAAAAATGCTCTTAATACA	2940
Qy	2941	AAAAA 2945	
Db	2941	AAAAA 2945	



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 1539 CTCACACATGACAGAGCGGGTGGACGCTGACGCGGAGTCCCGCTTCACTGAGG 1598  
 2155 AACGGAGACCTGTGACCAAGCAGCTGACAGATGGAAGATCTCCCGTGAAAGGTTT 2214  
 1599 AACGGAGACCTGTGACCAAGCAGCTGACAGATGGAAGATCTCCCGTGAAAGGTTT 1658  
 2215 GGTTTGAATGCCCCGGGGCAGCAAACTGACATGTTGAATGATAGCATTTCACTCTGC 2274  
 1659 GGTTTGAATGCCCCGGGGCAGCAAACTGACATGTTGAATGATAGCATTTCACTCTGC 1718  
 2275 GTTCTCTAGATCTGAGCAAGCTGTGAGTTCTCAACCCCAAGCTGATATATACATGAGCTA 2334  
 1719 GTTCTCTAGATCTGAGCAAGCTGTGAGTTCTCAACCCCAAGCTGATATATACATGAGCTA 1778  
 2335 ACTTTTTTAAATGTACAAAGCGCATCTCCAGATTCAGAGCCCTGCGCATGACTTTT 2394  
 1779 ACTTTTTTAAATGTACAAAGCGCATCTCCAGATTCAGAGCCCTGCGCATGACTTTT 1838  
 2395 CTTGAAGGCTTGCTTTTCCCTCGCTTCTGAAAGTGCATTTAGAGCGAGTCACTGGA 1898  
 1839 CTTGAAGGCTTGCTTTTCCCTCGCTTCTGAAAGTGCATTTAGAGCGAGTCACTGGA 2454  
 2455 GATCTCACTTTGCAATTTTGTGTTTACAGTGAAGCTTTTAAAGTCTCATCCAGCA 2514  
 1899 GCATCTCACTTTGCAATTTTGTGTTTACAGTGAAGCTTTTAAAGTCTCATCCAGCA 1958  
 2515 TTCTAATGCGAGGTTGCTGTAGGTTAACTTTTGAAGTATATATATCTGTTCTGCTA 2574  
 1959 TTCTAATGCGAGGTTGCTGTAGGTTAACTTTTGAAGTATATATATCTGTTCTGCTA 2018  
 2575 TCCTTAGTCTAATCTGCGGTACAGTAACTGAGATGTAAGTCTACCGTACTTCCCTCCCA 2634  
 2019 TCCTTAGTCTAATCTGCGGTACAGTAACTGAGATGTAAGTCTACCGTACTTCCCTCCCA 2078  
 2635 CACCATACGATAAAGCAAGACATTTTATACGATACCGAGTCACTATGTGTTCTCCCT 2694  
 2079 CACCATACGATAAAGCAAGACATTTTATACGATACCGAGTCACTATGTGTTCTCCCT 2138  
 2695 GAAATAACGATTCGAAATCCATGCGAGTATATTTTCTAAGTTTGGAAAGCAGG 2754  
 2139 GAAATAACGATTCGAAATCCATGCGAGTATATTTTCTAAGTTTGGAAAGCAGG 2198  
 2755 TTTTTTCTTTTAAATAATATAGACAGGTTCACTAAATTTAGTTAGTCAAGATTCCTA 2814  
 2199 TTTTTTCTTTTAAATAATATAGACAGGTTCACTAAATTTAGTTAGTCAAGATTCCTA 2258  
 2815 GACTGAAAGAACCTTAAACAAATAATTTTAAAGATATATATATATGCTGTATGTTA 2874  
 2259 GACTGAAAGAACCTTAAACAAATAATTTTAAAGATATATATATATGCTGTATGTTA 2318  
 2875 TGTAAATTTATTTAGGCTATAATACATTTCTCTATTTTTCGATTTTCAATAAATGCTCT 2934  
 2319 TGTAAATTTATTTAGGCTATAATACATTTCTCTATTTTTCGATTTTCAATAAATGCTCT 2378  
 2935 AATACAAA 2943









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; NAME/KEY: misc_feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature

Query Match
Best Local Similarity 1.5%; Score 43.2; DB 4; Length 1230025;
Matches 96; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 2710 AATCCATGAGGAGTATATTTCTAAGTTTGGAAAGCAGGTTTTTCTTTTAA 2769
Db 110233 AATCTTGAAATGAAGATCTTTTCAGATAGATGAGATGATTTTATATA 1109174
QY 2770 AATTATAGACGGTTCATAAATGATTAGTCAGAAATTCCTAGACTGAAGAACTA 2829
Db 1109173 AATGCTAAACCTGAAGAGGATCTCTGCTGAAATGTTTCTGAGATTCAGATCTTC 1109114
QY 2830 AACCAAAAATATTTTAAAGATATAATATATGCTGTATGTTATGTAATTTTATAG 2889
Db 1109113 AGAATAGCTGCTACTGCACTTCAGACTTTTAGGAGATCTGATGAATCTTTAAG 1109054
QY 2890 GCTA 2893
Db 1109053 GCCA 1109050

RESULT 7
US-09-489-039A-2573/c
; Sequence 2573, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2573
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2573

Query Match
Best Local Similarity 1.4%; Score 42.6; DB 4; Length 1302;
Matches 90; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1249 GTGGCTGATGACACTGAAGAAACCTTCGTCCTGCCCCAGCTCTGTGCTCGGATCAT 1308
Db 856 GTGATGCCAGCGGAGAGAGATCTTCGCTTCGCCAGCATGTGCTGGGATGTTTAT 797
QY 1309 GTGCTCATGCGACGCTCTGTGCTACCTTACCTGCGGGTGCAGGTGCGACCTGGG 1368
Db 796 TGGCCTTATGACATCCAGATCGTCTCCGCTCGCTGCGGATATTGGCGGGCGCTGTC 737
QY 1369 CGTGGGCTCCTCTCGCGGGCTTTGTTGGAGAAATCCACCATGTCGCC 1417
Db 736 GCGGGGCGAGATGAACCTCTGGGTACAAACCACTACCTGATGCC 688

RESULT 8
US-09-489-039A-2262
; Sequence 2262, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2573
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2573

Query Match
Best Local Similarity 1.4%; Score 42.6; DB 4; Length 640681;
Matches 105; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 2727 TATATTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTTAAAAAATATAGACACGTT 2786
Db 355415 TATATAAATACCTAGTAATAATAATAATTTATTTTATTAAGTTTCTTTAGTAAAT 355474
QY 2787 CACTAAATGATTTAGTCAGAAATTCCTAGACTGAAGAACTTAAACAAAAAATATTTTA 2846
Db 355475 AATTATAATAATTTTTTTTATAGTAAATATAGAAAAACATTAATATATTTTA 355534
QY 2847 AGATATAAATATGCTGTATATGTAATTTATTTAGGCTATAATACATTTCT 2906
Db 355535 AAAAAATGTTATATTTTAAACAGTTTTTATAAATCATTCCTCAAAACCGCAATTTAA 355594
QY 2907 ATTTGCGATTTTCAATAAAATGTCTTA 2935

GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2262
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2262

Query Match
Best Local Similarity 1.4%; Score 42.6; DB 4; Length 1617;
Matches 90; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1249 GTGGCTGATGACACTGAAGAAACCTTCGTCCTTCCCTCCAGCTCTGTGCTCGGATCAT 1308
Db 93 GTGATGCCAGCGGAGAAAGATCTTCGCTTCGCCAGCATGTGCTGGGATGTTTAT 152
QY 1309 CGTCTCATGCGACGCTCTGTGCTACCTTACCTGCGGGTGCAGGTGCGACCTGGG 1368
Db 153 TCCCTTATCGACATCCAGATCGTCTCGCTTCGCTGCGGATATTGGCGGGCTGTC 212
QY 1369 CGTGGGCTCCTCTCGCGGGCTTTGTTGGAGAAATCCACCATGTCGCC 1417
Db 213 GCGGGGCGAGATGAACCGTCTGGGTACAAACCACTACCTGATGCC 261

RESULT 9
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, YASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match
Best Local Similarity 1.4%; Score 42.6; DB 4; Length 640681;
Matches 105; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 2727 TATATTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTTAAAAAATATAGACACGTT 2786
Db 355415 TATATAAATACCTAGTAATAATAATAATTTATTTTATTAAGTTTCTTTAGTAAAT 355474
QY 2787 CACTAAATGATTTAGTCAGAAATTCCTAGACTGAAGAACTTAAACAAAAAATATTTTA 2846
Db 355475 AATTATAATAATTTTTTTTATAGTAAATATAGAAAAACATTAATATATTTTA 355534
QY 2847 AGATATAAATATGCTGTATATGTAATTTATTTAGGCTATAATACATTTCT 2906
Db 355535 AAAAAATGTTATATTTTAAACAGTTTTTATAAATCATTCCTCAAAACCGCAATTTAA 355594
QY 2907 ATTTGCGATTTTCAATAAAATGTCTTA 2935
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Db 377 WTTWACCYTTTWWKMMMYTTKRRRWRGKWTCTYTAWSKYVWYSRWKKGRAAMYK 318  
QY 2525 AGTTCCTGTAGGTAACCTTTTGAAGTAGATATATACCTGGTCTGTATCCTTAGTCA 2584  
Db 317 RRGKYNRAARATWTRAAAMYTWTYWKSGCWKSMWKMKRYKWKCCYWWRRKYC 258  
QY 2585 TAACCTGCGGTACAGTAATAGGAATGACTACGGTACTTCCCTCCACACCATACGA 2644  
Db 257 CMKRRRRGKRRARSYKSGSYVYKGGKGGTGKGGKAMSKGRRRATTTTYYK 198  
QY 2645 TAAAGCAGACATTTTATACGATACACAGTCACTATGTCTCTCCCTGAATAAGC 2704  
Db 197 KKWRSYWAARGKTTTKKWAAMMMCMWYMRSMYYIKWAAWKSCKWRKGGSSG 138  
QY 2705 ATTCGAATCCATGCAAGTACGATATATTTTCTAAAGTTTGGAAAGCAGGTTTTTCTT 2764  
Db 137 RYTWKRRGTGCMGRGRWYSRRRCHWYCTKGSMMAMMSGKKRAAMCCSKYYVTWMCMA 78  
QY 2765 TAAAAAATTTATAGACAC 2782  
Db 77 AAAAAATTTAAAAAMMRS 60

## RESULT 13

US-09-621-976-9783/c  
; Sequence 9783, Application US/09621976  
; Patent No. 6539063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Joberit, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 9783  
; LENGTH: 353  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-9783

Query Match 1.4%; Score 41.4; DB 4; Length 353;

Best Local Similarity 50.4%; Pred. No. 0.16; Mismatches 101; Indels 0; Gaps 0;

Matches 102; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 2728 ATATTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTTAAAAAATTATAGACAGGTC 2787  
Db 309 ATGTAATTTAAAGTTGCAATGAAGCAATTACAGAAATATAATATTGGTATATACCTCTC 250  
QY 2788 ACTAAATTTAGTATAGCAGATTCCTAGACTGAAGAACCTAAACAAAAAATATTAA 2847  
Db 249 TATACCTGAATGATTTCAATTAATAAATGATCTGATCTTTAAACATGAATATTC 190  
QY 2848 AGATATAAATATATGCTGTATGTATGTATTTTATTTAGGCTATATACATTTCTTA 2907  
Db 189 AGATATGATCTATCTCTCTATTTTAAAAAATCACTTTAGCAAGATATTTTACATA 130  
QY 2908 TTTTCGATTTTCAATAAATGT 2930  
Db 129 CAATAATGTATCTATTCAGTGT 107

## RESULT 14

US-10-204-708-73  
; Sequence 73, Application US/10204708  
; Patent No. 6677731  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENBROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

; TITLE OF INVENTION: by Assessing DNA Methylation  
; FILE REFERENCE: 5013.1012  
; CURRENT APPLICATION NUMBER: US/10/204,708  
; CURRENT FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: PCT/EP01/03971  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: DE 10019058.8  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: DE 10032529.7  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DE 10043826.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 98  
; SEQ ID NO 73  
; LENGTH: 5152  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-204-708-73

Query Match 1.4%; Score 41.4; DB 4; Length 5152;  
Best Local Similarity 53.0%; Pred. No. 0.81;  
Matches 133; Conservative 0; Mismatches 116; Indels 2; Gaps 2;

QY 2694 TGAATAACGCATTCGAATCCATCGCAGTCAGTATATTTTCTAAGTTTGGAAAGCAG 2753  
Db 3345 TGAATAATGTTATTTGTTATATTTTAAATAATTTTGTGTAAATATTTTAAATAT 3404  
QY 2754 GTTTTTCCTTTAAAAAATTATAGACACGGTTCCTAAATTTGTTAGTCAGAAATTCCT 2813  
Db 3405 TTCGTTAATATAAATAGTTTATTTTACGATTTTATTTAGT-ATTTAGAAAAAGAAAA 3463  
QY 2814 AGCTGAAGAACCTAAACAAAAAATATTTTAAAGATATAATA-TATGCTGTATATGT 2872  
Db 3464 AAGAAAAAGTAAATTAAGTGATTTTAAAGTATTTTAAATTAATTAATATGT 3523  
QY 2873 TATGTAATTTATTTTGGCTATATACATTTTCCATTTTCCATTTTCAATAAATGTCT 2932  
Db 3524 TATTTAGAAAAATAAGTGTTTTATATTTTATTTTAAAGGAGATTTTATTTAATTT 3583  
QY 2933 CTAATACAAAA 2943  
Db 3584 TTAATAAAGA 3594

## RESULT 15

US-09-014-583-1  
; Sequence 1, Application US/09014583  
; Patent No. 6140077  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, Takeshi  
; APPLICANT: SUZUKI, Tadashi  
; APPLICANT: TOKUDA, Junko  
; APPLICANT: KATO, No. 6140077uo  
; APPLICANT: SAKAI, Yasuyoshi  
; APPLICANT: MOCHIZUKI, Daisuke  
; APPLICANT: TAKAHASHI, Hitoshi  
; TITLE OF INVENTION: METHOD FOR PRODUCING PHYTASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

Mon Apr 26 07:58:59 2004

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/014,583

FILING DATE: 28-JAN-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 200398/96

FILING DATE: 30-JUL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 027066-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 734 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Candida boidinii

DEVELOPMENTAL STAGE: wild type

US-09-014-583-1

Query Match 1.4%; Score 41; DB 3; Length 734;

Best Local Similarity 49.3%; Pred.No. 0.32; Mismatches 110; Indels 0; Gaps 0;

Matches 107; Conservative 0;

QY 2728 ATATTTTCTAAGTTTGGAAAGCAGGTTTTTCTTTTAAAAAATTATAGACACGGTTC 2787

Db 429 AAAAATTATATTTAAATGAATTAATTCCTTTATTTTAAATAATATCGTTAATTCCTTTA 488

QY 2788 ACTAATTTGATTTAGTCAGNATTCCTAGACTGAAGACCTAAACAAAAATATTTTAA 2847

Db 489 AATTCATTTTATTTTAAATTCCTTTATCATAGTATCATATAACAATTTATTAACAT 548

QY 2848 AGATAAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTTA 2907

Db 549 AGATACACATTTATTTTATTTATCATATTTATTTTAAATATTTGATTATTTTAAAAA 608

QY 2908 TTTTCGATTTTCAATAAAATGCTCTAATACAAAAA 2944

Db 609 TAATATCTTAATTAATTAATTTTACGAATATACAAA 645

Search completed: April 25, 2004, 17:25:23

Job time : 230 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2004, 12:30:23 ; Search time 1123 Seconds  
(without alignments)  
11140.644 Million cell updates/sec

Title: US-09-978-188A-6  
Perfect score: 2945  
Sequence: 1 cgtcgcccgctgcccctc.....aatgtctataacacaaaaa 2945

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002s:\*  
7: Geneseq2003as:\*  
8: Geneseq2003bs:\*  
9: Geneseq2003cs:\*  
10: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2945	100.0	2945	2 AAZ33895	Aaz33895 Human PRO
2	2945	100.0	2945	3 AAC78459	Aac78459 Human PRO
3	2945	100.0	2945	6 ABK40261	Abk40261 cDNA enco
4	2945	100.0	2945	7 ACD42428	Acd42428 Novel hum
5	2945	100.0	2945	7 ACA63463	Ac63463 Novel hum
6	2945	100.0	2945	7 ACA71627	Ac71627 Human sec
7	2945	100.0	2945	7 ABX92267	Abx92267 cDNA enco
8	2945	100.0	2945	7 ACA66008	Ac66008 Human cDN
9	2945	100.0	2945	8 ADA24545	Ada24545 Novel hum
10	2945	100.0	2945	8 ACD29609	Acd29609 Novel hum
11	2945	100.0	2945	8 ADA12206	Ada12206 Human cDN
12	2945	100.0	2945	8 ACD29024	Acd29024 Novel hum
13	2945	100.0	2945	9 AD873512	Ad873512 Human PRO
14	2945	100.0	2945	9 AD876228	Ad876228 Human PRO
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16	2945	100.0	2945	9 ADC61414	Adc61414 Human cDN
17	2945	100.0	2945	9 ADC63378	Adc63378 Human cDN
18	2945	100.0	2945	9 ADC66478	Adc66478 Human cDN
19	2945	100.0	2945	9 ADC68602	Adc68602 Human cDN
20	2945	100.0	2945	9 ADC62662	Adc62662 Human cDN
21	2945	100.0	2945	9 ADC67727	Adc67727 Human cDN
22	2945	100.0	2945	9 ADC41047	Adc41047 Human cDN
23	2945	100.0	2945	9 ADC67102	Adc67102 Human cDN

24	2945	100.0	2945	9 ADC62038	Adc62038 Human cDN
25	2945	100.0	2945	9 ADC41671	Adc41671 Human cDN
26	2945	100.0	2945	9 ADE49040	Ade49040 Human cDN
27	2945	100.0	2945	9 ADE35094	Ade35094 Human cDN
28	2945	100.0	2945	9 ADE18208	Ade18208 Human cDN
29	2945	100.0	2945	9 ADD72823	Add72823 Human cDN
30	2945	100.0	2945	9 ADD72181	Add72181 Human cDN
31	2945	100.0	2945	9 ADE16832	Ade16832 Human cDN
32	2945	100.0	2945	10 ADE48340	Ade48340 Human cDN
33	2945	100.0	2945	10 ADE89441	Ade89441 Human cDN
34	2756.6	93.6	2986	4 AAI59695	Aai59695 Human pol
35	2756.6	93.6	2986	9 ADE09752	Ade09752 Novel DNA
36	2747.6	93.3	3139	4 AAI59099	Aai59099 Human pol
37	2543.2	86.4	2744	6 ABL90359	Abi90359 Human sec
38	2332.2	79.2	2572	3 AAA26379	Aaa26379 Human sec
39	2332.2	79.2	2572	7 ADA56105	Ada56105 Gene enco
40	2332.2	79.2	2572	7 ADA39918	Ada39918 Human sec
41	2332.2	79.2	2572	7 ACC50502	Acc50502 Human sec
42	2332.2	79.2	2572	7 ABZ71278	Abz71278 Human sec
43	2332.2	79.2	2572	8 ADB91184	Adb91184 Human sec
44	2332.2	79.2	2572	9 ADC73564	Adc73564 Human sec
45	2146.6	72.9	2748	3 AAC77393	Aac77393 Human ORF

ALIGNMENTS

RESULT 1  
AAZ33895  
ID AAZ33895 standard; cDNA; 2945 BP.  
XX  
AC AAZ33895;  
XX  
XX  
DT 07-DEC-1999 (first entry)  
XX  
DE Human PRO274 nucleotides sequence.

XX  
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
KW secreted protein; transmembrane protein; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9946281-A2.  
XX  
PD 16-SEP-1999.  
XX  
PF 08-MAR-1999; 99WO-US005028.  
XX  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077641P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 13-MAR-1998; 98US-0078004P.  
PR 17-MAR-1998; 98US-00040220.  
PR 20-MAR-1998; 98US-0078886P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 20-MAR-1998; 98US-0078936P.  
PR 20-MAR-1998; 98US-0078939P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 26-MAR-1998; 98US-0079656P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079689P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 30-MAR-1998; 98US-0079920P.  
PR 30-MAR-1998; 98US-0079923P.  
PR 31-MAR-1998; 98US-0080105P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080328P.  
PR 01-APR-1998; 98US-0080333P.  
PR 01-APR-1998; 98US-0080334P.  
PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081223P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081953P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.  
PR 21-APR-1998; 98US-0082700P.  
PR 22-APR-1998; 98US-0082704P.  
PR 22-APR-1998; 98US-0082804P.  
PR 23-APR-1998; 98US-0082767P.  
PR 23-APR-1998; 98US-0082796P.  
PR 27-APR-1998; 98US-0083336P.  
PR 28-APR-1998; 98US-0083322P.  
PR 28-APR-1998; 98US-0083392P.  
PR 29-APR-1998; 98US-0083493P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083500P.  
PR 29-APR-1998; 98US-0083545P.  
PR 29-APR-1998; 98US-0083554P.  
PR 29-APR-1998; 98US-0083558P.  
PR 29-APR-1998; 98US-0083559P.  
PR 30-APR-1998; 98US-0083742P.  
PR 05-MAY-1998; 98US-0084366P.  
PR 06-MAY-1998; 98US-0084414P.  
PR 06-MAY-1998; 98US-0084411P.  
PR 07-MAY-1998; 98US-0084598P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 07-MAY-1998; 98US-0084627P.  
PR 07-MAY-1998; 98US-0084637P.  
PR 07-MAY-1998; 98US-0084639P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 13-MAY-1998; 98US-0085323P.  
PR 13-MAY-1998; 98US-0085338P.  
PR 13-MAY-1998; 98US-0085392P.  
PR 15-MAY-1998; 98US-0085573P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085689P.  
PR 15-MAY-1998; 98US-0085697P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0085704P.  
PR 22-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086414P.  
PR 22-MAY-1998; 98US-0086430P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 11-SEP-1998; 98US-0100038P.  
XX (GETH ) GENENTECH INC.  
XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
XX WPI; 1999-551358/46.  
XX P-PSDB; AAY41686.  
XX New secreted and transmembrane polypeptides and their polynucleotides,  
PT useful for treating blood coagulation disorders, cancers and cellular  
adhesion disorders.  
XX Claim 2; Fig 3; 530pp; English.  
XX The present invention describes secreted and transmembrane polypeptides  
and their polynucleotides. The nucleotide sequences are useful as sources  
of probes, primers, for chromosome mapping, and for generation of  
antisenese sequences. They can also be used to create transgenic animals.  
The proteins can be used to treat a variety of diseases and disorders,  
depending on their function. Diseases that may be treated include blood  
coagulation disorders, cancers and cellular adhesion disorders. They may  
also be used to raise antibodies. AA233891 to AA234338, and AAY41685 to  
AAY41774 represent polynucleotide and polypeptide sequence given in the  
exemplification of the present invention  
XX Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 2945; DB 2; Length 2945;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGCTCGCCCGCTCGCCCTCGCTCCCGCAGAGTCCCTCGCGGAGCAGATGTGTG 60  
DB 1 CGCTCGCCCGCTCGCCCTCGCTCCCGCAGAGTCCCTCGCGGAGCAGATGTGTG 60  
QY 61 GGCTCAGCCACGCGCGGAGCTATGTGAAATCCCGGCGCTCACGCACTACTGCCCC 120  
DB 61 GGCTCAGCCACGCGCGGAGCTATGTGAAATCCCGGCGCTCACGCACTACTGCCCC 120  
QY 121 GATCCGGTCTTGCTGCTCCCTCGGCAATACCAATAGCATCGACTTCGGGAGCAGGC 180  
DB 121 GATCCGGTCTTGCTGCTCCCTCGGCAATACCAATAGCATCGACTTCGGGAGCAGGC 180  
QY 181 CTTGAAACCGGGCATTCGCTGTCAAGGAGGATGAGTCGAGATCGCGGAGCTACGG 240  
DB 181 CTTGAAACCGGGCATTCGCTGTCAAGGAGGATGAGTCGAGATCGCGGAGCTACGG 240  
QY 241 GCTGGGTACTCCCTCATGAAGTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGG 300  
DB 241 GCTGGGTACTCCCTCATGAAGTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGG 300  
QY 301 CCTGGTGTGTAACAGCAAGAGAGACAGAGCCAAAGCCGCTCTGTATGTTGTTGTC 360  
DB 301 CCTGGTGTGTAACAGCAAGAGAGACAGAGCCAAAGCCGCTCTGTATGTTGTTGTC 360  
QY 361 AGGGCCATCGCTCCGCTCTTTCACACACTGATAGTATAGTATTAGGATACAT 420  
DB 361 AGGGCCATCGCTCCGCTCTTTCACACACTGATAGTATAGTATTAGGATACAT 420  
QY 421 TATCAATAAACTGCACCATGTGACGAGTCGGTGGGAGCAAGACGAGAGGCGCTTCCT 480  
DB 421 TATCAATAAACTGCACCATGTGACGAGTCGGTGGGAGCAAGACGAGAGGCGCTTCCT 480  
QY 481 GTACCTCGCGCTTTCCTTTTCATGACGCAATGGCATGGACCCATGCTGGCATTCCT 540  
DB 481 GTACCTCGCGCTTTCCTTTTCATGACGCAATGGCATGGACCCATGCTGGCATTCCT 540  
QY 541 AAAACACAAATACAGATTTCTCTGCTGGATGTGCTCAATCTCAGATGTCTAGTCAGGT 600  
DB 541 AAAACACAAATACAGATTTCTCTGCTGGATGTGCTCAATCTCAGATGTCTAGTCAGGT 600  
QY 601 TGTGTTGTAGCAATTTGCTTTCAGATGACCTGGAAATGCGGGAGCCCTGCTCATCCC 660  
DB 601 TGTGTTGTAGCAATTTGCTTTCAGATGACCTGGAAATGCGGGAGCCCTGCTCATCCC 660  
QY 661 GATCCTCTCTGTATACATGGGCGCACTTGTGCTGCTGCACCCATGCTGGGCTACTA 720  
DB 661 GATCCTCTCTGTATACATGGGCGCACTTGTGCTGCTGCACCCATGCTGGGCTACTA 720  
QY 721 CAAGAACATTCAGACATATCCCTGACAGAAATGCGCGAGAGCTGGGGAGATGCAAC 780  
DB 721 CAAGAACATTCAGACATATCCCTGACAGAAATGCGCGAGAGCTGGGGAGATGCAAC 780

QY	781	AATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTAATTTCTGGCCACACAGAGAAT	840
DB	781	AATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTAATTTCTGGCCACACAGAGAAT	840
QY	841	CAGTGGCCTATTGTCAACCTCTTTGTTCCCGGACCTTGGTGGCAGTCTGCAGCCAC	900
DB	841	CAGTGGCCTATTGTCAACCTCTTTGTTCCCGGACCTTGGTGGCAGTCTGCAGCCAC	900
QY	901	AGAGGAGTGGCGAATTTGACAGCCACATACCTCTGGGTGCATGCCATACGGCTGGTT	960
DB	901	AGAGGAGTGGCGAATTTGACAGCCACATACCTCTGGGTGCATGCCATACGGCTGGTT	960
QY	961	GACGGAATCGTGTGTATCTGCTTTGCGATGTTTGGACACCCAAACGCTGCTGAGAAATCTT	1020
DB	961	GACGGAATCGTGTGTATCTGCTTTGCGATGTTTGGACACCCAAACGCTGCTGAGAAATCTT	1020
QY	1021	GAGCAGGAAACACAGTCAAGGAGCCACATCAAGAAAGTTCACCTTCGTCTGCATGGC	1080
DB	1021	GAGCAGGAAACACAGTCAAGGAGCCACATCAAGAAAGTTCACCTTCGTCTGCATGGC	1080
QY	1081	TCTGTCACTCAAGCTCTGTTTGGATGTTTGGACACCCAAACGCTGCTGAGAAATCTT	1140
DB	1081	TCTGTCACTCAAGCTCTGTTTGGATGTTTGGACACCCAAACGCTGCTGAGAAATCTT	1140
QY	1141	GATAGACATCATCGAGTGGACTTTGCTTTGCGAGAACTCTGTTGTTCTTTCGGAT	1200
DB	1141	GATAGACATCATCGAGTGGACTTTGCTTTGCGAGAACTCTGTTGTTCTTTCGGAT	1200
QY	1201	CTTCTCTCTTCCAGTTCAGTCAAGTGAAGGCGCATCTCACCGGGTGGCTGATGAC	1260
DB	1201	CTTCTCTCTTCCAGTTCAGTCAAGTGAAGGCGCATCTCACCGGGTGGCTGATGAC	1260
QY	1261	ACTGAGAAACCTTCGTCCTTGGCCAGCTCTGCTGGGATCATCGTCTCATCGC	1320
DB	1261	ACTGAGAAACCTTCGTCCTTGGCCAGCTCTGCTGGGATCATCGTCTCATCGC	1320
QY	1321	CAGCCTCGTGTCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT	1380
DB	1321	CAGCCTCGTGTCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT	1380
QY	1381	CCTGGCGGCTTTGTTGGAGAAATCCATGGTGGCCATCGCTGGTGTATGTTACCG	1440
DB	1381	CCTGGCGGCTTTGTTGGAGAAATCCATGGTGGCCATCGCTGGTGTATGTTACCG	1440
QY	1441	GAGCAGAAAGAGATGAGATGAGTCTGGCCACCGAGGGGAAAGACTCTGCCATGAC	1500
DB	1441	GAGCAGAAAGAGATGAGATGAGTCTGGCCACCGAGGGGAAAGACTCTGCCATGAC	1500
QY	1501	AGACATGCTCCGACAGAGGAGTGAAGATGAGATGAGATGAGATGAGATGAGAT	1560
DB	1501	AGACATGCTCCGACAGAGGAGTGAAGATGAGATGAGATGAGATGAGATGAGAT	1560
QY	1561	AGGACGGGACCCATGGGCTGAGGAGGAGTCAAGTCAAGTCAAGTCAAGTCAAGT	1620
DB	1561	AGGACGGGACCCATGGGCTGAGGAGGAGTCAAGTCAAGTCAAGTCAAGTCAAGT	1620
QY	1621	CTCTTCCCTCTCCATCGTATTGTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCT	1680
DB	1621	CTCTTCCCTCTCCATCGTATTGTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCT	1680
QY	1681	GGCCTTGATTAAGGTTTCGTGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCT	1740
DB	1681	GGCCTTGATTAAGGTTTCGTGCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCT	1740
QY	1741	GGGGACCTTAGTGAATGTTCTTACTGTTGCTATGTAAAGAAACAAACGAAACACTG	1800
DB	1741	GGGGACCTTAGTGAATGTTCTTACTGTTGCTATGTAAAGAAACAAACGAAACACTG	1800
QY	1801	CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCAGCGTTGACGTTGTGTC	1860
DB	1801	CATACCCCTGCTCAGGAAACCCAAAGACACAGCTGCTCAGCGTTGACGTTGTGTC	1860

QY	1861	TCCTCCCTCGACAAATCTCTCTTTGGAAACCAAGGACTGCAGCTGTGCCATCGGCTCG	1920
DB	1861	TCCTCCCTCGACAAATCTCTCTTTGGAAACCAAGGACTGCAGCTGTGCCATCGGCTCG	1920
QY	1921	GTCAACCTTGACAGAGGACACAGACTCTCTCTGTCGCCCTTCATCGCTTTAAGAAATCAA	1980
DB	1921	GTCAACCTTGACAGAGGACACAGACTCTCTCTGTCGCCCTTCATCGCTTTAAGAAATCAA	1980
QY	1981	CAGGTTAAATCTCGGCTTCTTTGATTTGCTTCCAGTCACTGCGGTACAAAGAGATG	2040
DB	1981	CAGGTTAAATCTCGGCTTCTTTGATTTGCTTCCAGTCACTGCGGTACAAAGAGATG	2040
QY	2041	GAGCCCGGCTGCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCACTACTCCAC	2100
DB	2041	GAGCCCGGCTGCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCACTACTCCAC	2100
QY	2101	ACATGACAGAGGCGGTGGCGCTGCGAGCCCGGAGTCCCCGTTTACACTGAGGACCGA	2160
DB	2101	ACATGACAGAGGCGGTGGCGCTGCGAGCCCGGAGTCCCCGTTTACACTGAGGACCGA	2160
QY	2161	GACCTGTGACACACAGAGGCTGACAGATGGAAGTTCCTCCGTAGAAAGGTTTGGTTG	2220
DB	2161	GACCTGTGACACACAGAGGCTGACAGATGGAAGTTCCTCCGTAGAAAGGTTTGGTTG	2220
QY	2221	AAATGCCCGGGGAGCAAACTGACATGGTTGAATGATGATTTCACTCTGCGTTCTC	2280
DB	2221	AAATGCCCGGGGAGCAAACTGACATGGTTGAATGATGATTTCACTCTGCGTTCTC	2280
QY	2281	CTAGATCTGAGCAAGCTGTCACTCTCCGCCAGGATGAGAGTCTCCGTAGAAAGT	2340
DB	2281	CTAGATCTGAGCAAGCTGTCACTCTCCGCCAGGATGAGAGTCTCCGTAGAAAGT	2340
QY	2341	TTAAATTTGTCAAAAGGCGCATCTCCAGATTCAGACCTCGCGCATGACTTTTCTGAA	2400
DB	2341	TTAAATTTGTCAAAAGGCGCATCTCCAGATTCAGACCTCGCGCATGACTTTTCTGAA	2400
QY	2401	GGTTGCTTTTCCCTCGCCTTCTGAGAGTGCATGAGGAGTGCATGAGGAGTCC	2460
DB	2401	GGTTGCTTTTCCCTCGCCTTCTGAGAGTGCATGAGGAGTGCATGAGGAGTCC	2460
QY	2461	TAACTTTGCACTTTTGTGTTTAACTGAGTGAAGCTTAAAGTCTCATCCAGCATCTAA	2520
DB	2461	TAACTTTGCACTTTTGTGTTTAACTGAGTGAAGCTTAAAGTCTCATCCAGCATCTAA	2520
QY	2521	TGCCAGGTTGCTGTAGGTAACCTTTTGAAGTGAATATTTAGTGGTCTGCTATCTTA	2580
DB	2521	TGCCAGGTTGCTGTAGGTAACCTTTTGAAGTGAATATTTAGTGGTCTGCTATCTTA	2580
QY	2581	GTCAATCTCTGCGGTACAGGTAATGAGAAATGTAAGTACTTCCCTCCACACCAT	2640
DB	2581	GTCAATCTCTGCGGTACAGGTAATGAGAAATGTAAGTACTTCCCTCCACACCAT	2640
QY	2641	ACGATAAGCAAGACATTTTATAACGATACAGAGTCACTATGCGTCTCCCTGAAATA	2700
DB	2641	ACGATAAGCAAGACATTTTATAACGATACAGAGTCACTATGCGTCTCCCTGAAATA	2700
QY	2701	ACGATTTGCAAAATCCATGAGTGCATATTTTCTAAAGTTTGGAAAGCAGGTTTTT	2760
DB	2701	ACGATTTGCAAAATCCATGAGTGCATATTTTCTAAAGTTTGGAAAGCAGGTTTTT	2760
QY	2761	CTTTTAAAGAAATTTAGACACGGTTTCACTAAATGATTTAGTCAAGATTCCTAGACTGA	2820
DB	2761	CTTTTAAAGAAATTTAGACACGGTTTCACTAAATGATTTAGTCAAGATTCCTAGACTGA	2820
QY	2821	AAGAACTTAAACAAAGAAATTTTAAAGATATAATATGCTGATATGTTATGTAAT	2880
DB	2821	AAGAACTTAAACAAAGAAATTTTAAAGATATAATATGCTGATATGTTATGTAAT	2880
QY	2881	TTATTTTAGGCTATAATACATTTTCTTATTTTCCATTTTCAATTAATAATGCTCTAATA	2940
DB	2881	TTATTTTAGGCTATAATACATTTTCTTATTTTCCATTTTCAATTAATAATGCTCTAATA	2940
QY	2941	AAAAA	2945







KW inflammatory disorder; immune disorder; angiogenic disorder;  
KW gene therapy; cytostatic; neuroprotective; gene; ss.  
XX Homo sapiens.  
OS WO200153486-A1.  
PN XX  
PD XX  
XX 26-JUL-2001.  
XX  
XX 11-FEB-2000; 2000WO-US003565.  
XX  
XX 08-MAR-1999; 99WO-US005028.  
XX 11-MAR-1999; 99US-0123972P.  
XX 11-MAY-1999; 99US-0133459P.  
XX 02-JUN-1999; 99WO-US012252.  
XX 22-JUN-1999; 99US-0140650P.  
XX 22-JUN-1999; 99US-0140653P.  
XX 20-JUL-1999; 99US-0144758P.  
XX 26-JUL-1999; 99US-0145698P.  
XX 28-JUL-1999; 99US-0146222P.  
XX 17-AUG-1999; 99US-0149395P.  
XX 31-AUG-1999; 99US-0151689P.  
XX 01-SEP-1999; 99WO-US020111.  
XX 15-SEP-1999; 99WO-US021090.  
XX 30-NOV-1999; 99WO-US028313.  
XX 01-DEC-1999; 99WO-US028301.  
XX 01-DEC-1999; 99WO-US028634.  
XX 05-JAN-2000; 2000WO-US000219.  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Goddard A, Godowski RJ, Gurney AL, Hillan KJ;  
PI Marschers SA, Pan J, Picti RM, Roy NA, Smith V, Stone DM;  
PI Watanabe CK, Wood WI;  
XX  
XX WPI; 2002-205567/36.  
DR P-PSDB; AAUS6135.  
XX  
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
PT benign or malignant tumors, leukemias and lymphoid malignancies,  
PT inflammatory, angiogenic and immunologic disorders.  
XX  
XX Claim 50; Fig 15; 302pp; English.

XX The present invention relates to the isolation of novel human PRO  
CC polypeptides and the polynucleotide sequences encoding them. The PRO  
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for  
CC treating benign or malignant tumors (e.g. renal, kidney, bladder,  
CC breast, etc), leukaemias and lymphoid malignancies, other disorders such  
CC as neuronal, gliat, astrocytal, hypothalamic, glandular, macrophagal,  
CC stromal and blastocoeleic disorders, inflammatory, immune and angiogenic  
CC disorders. The polynucleotide sequences are also useful in gene therapy.  
CC ABK40254-ABK40288 encode for the human PRO polypeptides of the invention  
XX  
XX Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;

Query Match 100.0%; Score 2945; DB 6; Length 2945;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCCGCGCGTCCGCTCCGCTCCGCGAGTCCCTCCGCGGAGAGATGTGTG 60  
DB 1 CGTCCGCGCGTCCGCTCCGCTCCGCGAGTCCCTCCGCGGAGAGATGTGTG 60  
QY 61 GGGTCAGCCACGCGCGGAGTATGTGAAATCCCGGCGCTCAGCACTACTGGCCCT 120  
DB 61 GGGTCAGCCACGCGCGGAGTATGTGAAATCCCGGCGCTCAGCACTACTGGCCCT 120  
QY 121 GATCCGGTTTGGTGGCCCTGGGCATCACCACATAGGCATCGACTTCGGGAGAGGC 180  
DB 121 GATCCGGTTTGGTGGCCCTGGGCATCACCACATAGGCATCGACTTCGGGAGAGGC 180  
QY 181 CTTGAACCGGGGCAATTGCTGCTCAAGGAGGATGAGTCGATGCTGCCAGCTACCG 240

DB 181 CTTGAACCGGGGCAATTGCTGCTCAAGGAGGATGAGTCGATGCTGCCAGCTACCG 240  
QY 241 GCTGGCGTACTCCCTCATGAAGTTCTTACGGGTCCCATAGTGAATTCAAAATGTGG 300  
DB 241 GCTGGCGTACTCCCTCATGAAGTTCTTACGGGTCCCATAGTGAATTCAAAATGTGG 300  
QY 301 CTTGGTGTGTGAACAGCAAGAGAGACAGACCAAGCCGCTCTGTGTATGTGTGGTGGC 360  
DB 301 CTTGGTGTGTGAACAGCAAGAGAGAGACCAAGCCGCTCTGTGTATGTGTGGTGGC 360  
QY 361 AGGGCCCATCGCTCCGCTTTTACACACTGATAGTTATAGTGAATTTAGGATACTACAT 420  
DB 361 AGGGCCCATCGCTCCGCTTTTACACACTGATAGTTATAGTGAATTTAGGATACTACAT 420  
QY 421 TATCAATAAACTGACCATGTGACGAGTGGTGGGAGCAAGCAGAGAGGGCCCTTCT 480  
DB 421 TATCAATAAACTGACCATGTGACGAGTGGTGGGAGCAAGCAGAGAGGGCCCTTCT 480  
QY 481 GTACCTCGCCGCTTTTCTTTTATGAGCAAGCAATGGCATGCCATCTGTGGCAATCTCTT 540  
DB 481 GTACCTCGCCGCTTTTCTTTTATGAGCAAGCAATGGCATGCCATCTGTGGCAATCTCTT 540  
QY 541 AAACACAAATACAGTTTCTTCTGCTGGGATGTGCTCAATCTCAGATGTCTAGCTCAGGT 600  
DB 541 AAACACAAATACAGTTTCTTCTGCTGGGATGTGCTCAATCTCAGATGTCTAGCTCAGGT 600  
QY 601 TGTITTTGTAGCCATTTTGTCTTACAGTCACTCCGGAATGCCGGAGGCCCTGTCTATCCC 660  
DB 601 TGTITTTGTAGCCATTTTGTCTTACAGTCACTCCGGAATGCCGGAGGCCCTGTCTATCCC 660  
QY 661 GATCCTCTCTTTAGATGAGTGGGCGCTTGTGGGCTTAAATTTCTGGCCACACAGAGAT 720  
DB 661 GATCCTCTCTTTAGATGAGTGGGCGCTTGTGGGCTTAAATTTCTGGCCACACAGAGAT 720  
QY 721 CAAGAACATTCAGACATCATCTTCAAGAAAGTGGCCCGGAGCTGGGGGAGATCAAC 780  
DB 721 CAAGAACATTCAGACATCATCTTCAAGAAAGTGGCCCGGAGCTGGGGGAGATCAAC 780  
QY 781 AATGAAGAAATGCTGAGCTTCTGGTGGCCCTTTGGTCTTAAATTTCTGGCCACACAGAGAT 840  
DB 781 AATGAAGAAATGCTGAGCTTCTGGTGGCCCTTTGGTCTTAAATTTCTGGCCACACAGAGAT 840  
QY 841 CAGTCCGCTTATGTCAACCTTTTGTTCGCGGAGCTTGTGGGAGTCTCAGCCAC 900  
DB 841 CAGTCCGCTTATGTCAACCTTTTGTTCGCGGAGCTTGTGGGAGTCTCAGCCAC 900  
QY 901 AGAGCGAGTGGGATTTTGAAGCAGCATACCTGTGGGTCAATGCCATACGGCTGGTT 960  
DB 901 AGAGCGAGTGGGATTTTGAAGCAGCATACCTGTGGGTCAATGCCATACGGCTGGTT 960  
QY 961 GACGGAATCCGTGCTGTATCTGCTTTCGACAAAGATTAACCCAGCAACAACTGGT 1020  
DB 961 GACGGAATCCGTGCTGTATCTGCTTTCGACAAAGATTAACCCAGCAACAACTGGT 1020  
QY 1021 GAGCAAGCAACACAGTACGCGAGCCACATCAAGAAAGTTCACTTCTGTGCAATGGC 1080  
DB 1021 GAGCAAGCAACACAGTACGCGAGCCACATCAAGAAAGTTCACTTCTGTGCAATGGC 1080  
QY 1081 TCTGTCACTACGCTCGTTTCTGTTTTCGACACCAACAGTGTCTGAGAAATCTT 1140  
DB 1081 TCTGTCACTACGCTCGTTTCTGTTTTCGACACCAACAGTGTCTGAGAAATCTT 1140  
QY 1141 GATAGACATCATCGGAGTGGACTTTGCTTTTGCAGAACTCTGTGTGTCTCTTTGGGAT 1200  
DB 1141 GATAGACATCATCGGAGTGGACTTTGCTTTTGCAGAACTCTGTGTGTCTCTTTGGGAT 1200  
QY 1201 CTTTCTCTTCTTCCAGTCCAGTCAAGTGGGCGCATCTCACCGGGTGGTGTGAC 1260  
DB 1201 CTTTCTCTTCTTCCAGTCCAGTCAAGTGGGCGCATCTCACCGGGTGGTGTGAC 1260  
QY 1261 ACTGAAGAAACCTTCTCTTCTGCCCCAGCTCTGTGCTCGGATCATCTCTCTATCGC 1320

Db 1261 ACTGAAGAAAACCTTCGTCTGCCCCAGCTCTGTCTGGGATCATGTCTCATCGC 1320  
Qy 1321 CAGCCTCGTGTCTACCTACCTGCGGGTGCACGGTGCACCCCTGGGCGTGGCTCCCT 1380  
Db 1321 CAGCCTCGTGTCTACCTACCTGCGGGTGCACGGTGCACCCCTGGGCGTGGCTCCCT 1380  
Qy 1381 CCTGGCGGCTTTCTGGGAGAAATCCACATCGTGCCTCGCTGCGTGCCTATGCTACCG 1440  
Db 1381 CCTGGCGGCTTTCTGGGAGAAATCCACATCGTGCCTCGCTGCGTGCCTATGCTACCG 1440  
Qy 1441 GAACAGAAAAGAGATGGAGATGAGTGGCCACCGAGGGGGAAGACTTCGCCATGAC 1500  
Db 1441 GAACAGAAAAGAGATGGAGATGAGTGGCCACCGAGGGGGAAGACTTCGCCATGAC 1500  
Qy 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGATGAATA 1560  
Db 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGATGAATA 1560  
Qy 1561 AGGACGGGACGCCATGGGCACTCGAGGACGGTCACTGAGGATGACACTTCGGCATCAT 1620  
Db 1561 AGGACGGGACGCCATGGGCACTCGAGGACGGTCACTGAGGATGACACTTCGGCATCAT 1620  
Qy 1621 CTCCTCCCTCCCATCGTATTTGTTCCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1680  
Db 1621 CTCCTCCCTCCCATCGTATTTGTTCCCTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 1680  
Qy 1681 GGCCTTGATTTAAAGGTTTCGTCAATTCCTAGCATCTGCTGAGGATGACACTTCGGCATCAT 1740  
Db 1681 GGCCTTGATTTAAAGGTTTCGTCAATTCCTAGCATCTGCTGAGGATGACACTTCGGCATCAT 1740  
Qy 1741 GGGGACCTAGTGAATGCTTTACTGTTGCTATGTAAGAAACCAACCAACCAACCAACCAACCA 1800  
Db 1741 GGGGACCTAGTGAATGCTTTACTGTTGCTATGTAAGAAACCAACCAACCAACCAACCAACCA 1800  
Qy 1801 CATACCCCTGCTCAGCAAAACCCAAAGACACAGCTGCTCAGCGTTGAGTTGTCTCC 1860  
Db 1801 CATACCCCTGCTCAGCAAAACCCAAAGACACAGCTGCTCAGCGTTGAGTTGTCTCC 1860  
Qy 1861 TCCTCCCTGACAAATCTCTTGGAAACCAAGGACTGAGCTGTGCGATCGCGCTCG 1920  
Db 1861 TCCTCCCTGACAAATCTCTTGGAAACCAAGGACTGAGCTGTGCGATCGCGCTCG 1920  
Qy 1921 GTCACCTGCAAGAGCCACAGACTCTCTGTCCTCCCTTCATCGCTCTTAAGAAACAA 1980  
Db 1921 GTCACCTGCAAGAGCCACAGACTCTCTGTCCTCCCTTCATCGCTCTTAAGAAACAA 1980  
Qy 1981 CAGTTTAAATCTCGGCTTCCTTTGATTTGCTTCCAGTCAATGCGCGTACAAAGAGATG 2040  
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## RESULT 4

ACD42428  
ID ACD42428 standard; cDNA; 2945 BP.

XX ACD42428;

XX DT 09-SEP-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO274 cDNA.

XX KW Human; secreted and transmembrane protein; PRO; virucide; gene therapy;  
XX XN cell death; growth induction cascade; blood coagulation cascade;  
XX XW viral infection; gene; ss.

XX OS Homo sapiens.

XX PN US2003050239-A1.

XX PD 13-MAR-2003.

XX PF 15-OCT-2001; 2001US-00978191.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 03-NOV-1997; 97US-0064249P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 21-NOV-1997; 97US-0066364P.

XX PR 10-MAR-1998; 98US-0077450P.

XX PR 11-MAR-1998; 98US-0077632P.

XX PR 11-MAR-1998; 98US-0077641P.

XX PR 11-MAR-1998; 98US-0077649P.

XX PR 12-MAR-1998; 98US-0077791P.

PR	13-MAR-1998;	98US-0078004P.	PR	15-MAY-1998;	98US-0085704P.
PR	17-MAR-1998;	98US-00040220.	PR	18-MAY-1998;	98US-0086032P.
PR	20-MAR-1998;	98US-0078886P.	PR	22-MAY-1998;	98US-0086392P.
PR	20-MAR-1998;	98US-0078910P.	PR	22-MAY-1998;	98US-0086414P.
PR	20-MAR-1998;	98US-0078936P.	PR	22-MAY-1998;	98US-0086430P.
PR	20-MAR-1998;	98US-0078939P.	PR	22-MAY-1998;	98US-0086486P.
PR	25-MAR-1998;	98US-0079294P.	PR	28-MAY-1998;	98US-0087098P.
PR	26-MAR-1998;	98US-0079656P.	PR	28-MAY-1998;	98US-0087106P.
PR	27-MAR-1998;	98US-0079663P.	PR	28-MAY-1998;	98US-0087208P.
PR	27-MAR-1998;	98US-0079664P.	PR	26-JUN-1998;	98US-00105413.
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PR	27-MAR-1998;	98US-0079786P.	PR	01-JUL-1998;	98US-0091359P.
PR	30-MAR-1998;	98US-0079920P.	PR	30-JUL-1998;	98US-0094651P.
PR	30-MAR-1998;	98US-0079923P.	PR	11-SEP-1998;	98US-00100038P.
PR	31-MAR-1998;	98US-0080105P.	PR	07-OCT-1998;	98US-00168978.
PR	31-MAR-1998;	98US-0080107P.	PR	07-OCT-1998;	98US-00211141.
PR	31-MAR-1998;	98US-0080165P.	PR	02-NOV-1998;	98US-00184216.
PR	31-MAR-1998;	98US-0080194P.	PR	06-NOV-1998;	98US-00187368.
PR	01-APR-1998;	98US-0080327P.	PR	20-NOV-1998;	98US-0093040P.
PR	01-APR-1998;	98US-0080333P.	PR	20-NOV-1998;	98US-00942855.
PR	01-APR-1998;	98US-0080334P.	PR	27-DEC-1998;	98US-00202054.
PR	08-APR-1998;	98US-0081049P.	PR	22-DEC-1998;	98US-00218517.
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PR	09-APR-1998;	98US-0081195P.	PR	23-DEC-1998;	98US-0113621P.
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PR	15-APR-1998;	98US-0081817P.	PR	08-MAR-1999;	98US-00254465.
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PR	15-APR-1998;	98US-0081838P.	PR	10-MAR-1999;	98US-00254465.
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PR	21-APR-1998;	98US-0082568P.	PR	29-MAR-1999;	98US-0126773P.
PR	21-APR-1998;	98US-0082569P.	PR	12-APR-1999;	98US-00284291.
PR	22-APR-1998;	98US-0082704P.	PR	21-APR-1999;	98US-0130232P.
PR	22-APR-1998;	98US-0082804P.	PR	28-APR-1999;	98US-0131032P.
PR	23-APR-1998;	98US-0082736P.	PR	28-APR-1999;	98US-0131445P.
PR	27-APR-1998;	98US-0083334P.	PR	14-MAY-1999;	98US-00311832.
PR	28-APR-1998;	98US-0083332P.	PR	14-MAY-1999;	98US-0134287P.
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PR	29-APR-1998;	98US-0083499P.	PR	16-JUN-1999;	98US-0139557P.
PR	29-APR-1998;	98US-0083500P.	PR	23-JUN-1999;	98US-0141037P.
PR	29-APR-1998;	98US-0083545P.	PR	07-JUL-1999;	98US-0142680P.
PR	29-APR-1998;	98US-0083554P.	PR	28-JUL-1999;	98US-0145698P.
PR	29-APR-1998;	98US-0083559P.	PR	25-AUG-1999;	98US-0146224P.
PR	29-APR-1998;	98US-0083559P.	PR	25-AUG-1999;	98US-00380137.
PR	30-APR-1998;	98US-0083742P.	PR	25-AUG-1999;	98US-00380138.
PR	06-MAY-1998;	98US-0084414P.	PR	25-AUG-1999;	98US-00380142.
PR	06-MAY-1998;	98US-0084441P.	PR	29-OCT-1999;	98US-0162506P.
PR	07-MAY-1998;	98US-0084598P.	PR	30-NOV-1999;	98US-0162506P.
PR	07-MAY-1998;	98US-0084600P.	PR	02-DEC-1999;	98US-0162506P.

27-NOV-2000; 2000US-00723749.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 22-MAR-2001; 2001US-00816920.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 30-JUL-2001; 2001US-00918585.  
XX  
(GETH ) GENENTECH INC.  
XX  
Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;  
PI Ferrara N, Filvaroff E, Fong S, Gao M, Gerber H, Gerritsen ME;  
PI  
Query Match 100.0%; Score 2945; DB 7; Length 2945;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGCTGCCCGCTGCGCCCTCGCTCCCGCAGATCCCTCGCGGACGAGATGTGTG 60  
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09-APR-1998; 98US-0081195P.  
09-APR-1998; 98US-0081203P.  
09-APR-1998; 98US-0081229P.  
15-APR-1998; 98US-0081817P.  
15-APR-1998; 98US-0081819P.  
15-APR-1998; 98US-0081838P.  
15-APR-1998; 98US-0081952P.  
15-APR-1998; 98US-0081955P.  
21-APR-1998; 98US-0082568P.  
21-APR-1998; 98US-0082569P.  
22-APR-1998; 98US-0082700P.  
22-APR-1998; 98US-0082704P.  
22-APR-1998; 98US-0082804P.  
22-APR-1998; 98US-0082804P.  
23-APR-1998; 98US-0082796P.  
07-OCT-1998; 98WO-US021141.  
20-NOV-1998; 98WO-US024855.  
05-JAN-1999; 99WO-US000106.  
08-MAR-1999; 99WO-US005028.  
10-MAR-1999; 99WO-US005190.  
14-MAY-1999; 99WO-US010733.  
02-JUN-1999; 99WO-US012252.  
30-NOV-1999; 99WO-US028313.  
02-DEC-1999; 99WO-US028551.  
02-DEC-1999; 99WO-US028565.  
16-DEC-1999; 99WO-US030095.  
30-DEC-1999; 99WO-US031243.  
30-DEC-1999; 99WO-US031274.  
03-JAN-2000; 2000WO-US000219.  
06-JAN-2000; 2000WO-US000277.  
06-JAN-2000; 2000WO-US000376.  
11-FEB-2000; 2000WO-US003565.  
18-FEB-2000; 2000WO-US004341.  
24-FEB-2000; 2000WO-US005004.  
02-MAR-2000; 2000WO-US005841.  
10-MAR-2000; 2000WO-US006319.  
21-MAR-2000; 2000WO-US007532.  
30-MAR-2000; 2000WO-US008439.  
17-MAY-2000; 2000WO-US013705.  
22-MAY-2000; 2000WO-US014042.  
30-MAY-2000; 2000WO-US014941.  
02-JUN-2000; 2000WO-US015264.  
28-JUL-2000; 2000WO-US020710.  
24-AUG-2000; 2000WO-US023328.  
01-DEC-2000; 2000WO-US032678.  
20-DEC-2000; 2000WO-US034956.  
28-FEB-2001; 2001WO-US006520.  
22-MAR-2001; 2001WO-US009552.  
25-MAY-2001; 2001WO-US017092.  
01-JUN-2001; 2001WO-US017800.  
20-JUN-2001; 2001WO-US019592.  
29-JUN-2001; 2001WO-US021066.  
09-JUL-2001; 2001WO-US021735.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
KlJavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;  
Stewart TA, Tumas D, Williams PM, Wood WI;  
WPI, 2003-328860/31.  
P-PSDB; ASU72194.  
New secreted and transmembrane nucleic acids and polypeptides, designated  
as PRO, useful for treating inflammation, organ failure, atherosclerosis,  
cardiac injury, infertility, birth defects, premature aging, AIDS, or  
cancer.  
Claim 2; Fig 3; 453pp; English.  
The invention describes an isolated nucleic acid (I) comprising, or which

is at least 80 % sequence identity to, or the full-length coding sequence  
of, any of 118 300-2100 nucleotide sequences, which encodes its  
corresponding PRO polypeptide selected from 118 100-700 amino acid  
sequences, all given in the specification. The nucleic acids and  
polypeptides are useful for treating inflammatory diseases, organ  
failure, atherosclerosis, cardiac injury, infertility, birth defects,  
premature aging, AIDS, cancer, or diabetic complications. The nucleic  
acids are useful as hybridisation probes, in chromosome and gene mapping,  
and in generating antisense RNA or DNA. The polypeptides are useful as  
pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful  
in tissue typing. This sequence encodes a novel human secreted and  
transmembrane PRO polypeptide  
XX Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;  
Query Match 100.0%; Score 2945; DB 7; Length 2945;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 601 TGTGTTTGTAGCCATTTGCTTTCAGTCAAGTCAAGTCCGAGAGCCCTGCTCATCC 660  
QY 661 GATCCTCTCCTTGTATACATGGGCGCACTTGTGGCTGCGACCCCTGTGCTGGGTACTA 720  
DB 661 GATCCTCTCCTTGTATACATGGGCGCACTTGTGGCTGCGACCCCTGTGCTGGGTACTA 720  
QY 721 CAAGAACATTCAGACATCATCCCTGACAGAGTGGCCGAGCTGGGGAGATGCAAC 780  
DB 721 CAAGAACATTCAGACATCATCCCTGACAGAGTGGCCGAGCTGGGGAGATGCAAC 780  
QY 781 AATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTTAATTTCTGGCCACACAGAGAT 840  
DB 781 AATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTTAATTTCTGGCCACACAGAGAT 840



Db 781 AATAAGAAAGATGCTGAGCTTCTGGTGGCTTTGGCTCTTAATTCTGGCCACACAGAGAT 840  
Qy 841 CAGTCGGCTATATGTCACACTCTTTGTTCCCGGACCTTGGTGGCACTCTGGTGGCACTCTGAGCCAC 900  
Db 841 CAGTCGGCTATATGTCACACTCTTTGTTCCCGGACCTTGGTGGCACTCTGGTGGCACTCTGAGCCAC 900  
Qy 901 AGAGGAGTGGGCAATTTGACAGCCACATACCCTCTGGGTGCATGCGATACGGCTGGTT 960  
Db 901 AGAGGAGTGGGCAATTTGACAGCCACATACCCTCTGGGTGCATGCGATACGGCTGGTT 960  
Qy 961 GAGGAAATCCGTCGTGTATCCTCTTTCGACAGAGATACCCGACGACAACTGGT 1020  
Db 961 GAGGAAATCCGTCGTGTATCCTCTTTCGACAGAGATACCCGACGACAACTGGT 1020  
Qy 1021 GAGCAGAGCAACACAGTCAAGGAGCCACATCAAGAGTTTCACTTCTGTCATGGC 1080  
Db 1021 GAGCAGAGCAACACAGTCAAGGAGCCACATCAAGAGTTTCACTTCTGTCATGGC 1080  
Qy 1081 TCTGTCACTCACCTCTCTTCTGATGTTTGGACACCCACGTTCTGAGAGAAATCTT 1140  
Db 1081 TCTGTCACTCACCTCTCTTCTGATGTTTGGACACCCACGTTCTGAGAGAAATCTT 1140  
Qy 1141 GATAGACATCATCGAGTGAATTTGCTTTCGAGAACTCTGTGTGTTCTTTCGGAT 1200  
Db 1141 GATAGACATCATCGAGTGAATTTGCTTTCGAGAACTCTGTGTGTTCTTTCGGAT 1200  
Qy 1201 CTCTCTCTTCTCCAGTTCCAGTCAAGTGGGGCGCATCTCACCGGTTGGCTGATGAC 1260  
Db 1201 CTCTCTCTTCTCCAGTTCCAGTCAAGTGGGGCGCATCTCACCGGTTGGCTGATGAC 1260  
Qy 1261 ACTGAGAAATCTCTGCTTCTGCTTCCGCTCTGCTGCGGATCATGCTCTCATGCG 1320  
Db 1261 ACTGAGAAATCTCTGCTTCTGCTTCCGCTCTGCTGCGGATCATGCTCTCATGCG 1320  
Qy 1321 CAGCTCTGCTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 1380  
Db 1321 CAGCTCTGCTCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTT 1380  
Qy 1381 CTTGGGGGCTTGTGGGAGATTCACATGTTGGCCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
Db 1381 CTTGGGGGCTTGTGGGAGATTCACATGTTGGCCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
Qy 1441 GAAGCAGAAAGAAAGATGAGATGAGTTCGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Db 1441 GAAGCAGAAAGAAAGATGAGATGAGTTCGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
Qy 1501 AGACATGCTCCGACAGAGAGTGAAGACATTCGTTGGAATGAGAGAGGAGGAGGAGGAGGAG 1560  
Db 1501 AGACATGCTCCGACAGAGAGTGAAGACATTCGTTGGAATGAGAGAGGAGGAGGAGGAGGAG 1560  
Qy 1561 AGGACAGGAGCGCATGGGCACTGCGAGGAGCGGTCACTCAGGATGACACTTCGGCATCAT 1620  
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Qy 1621 CTCTTCCCTCTCCGATGATTTGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1680  
Db 1621 CTCTTCCCTCTCCGATGATTTGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1680  
Qy 1681 GGGCTTGATTTAAGGTTTCTGTCATCTCTGACATGCTGGGTATGCTCAGCTGACG 1740  
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Qy 1741 GGGGACCTAGTGAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1800  
Db 1741 GGGGACCTAGTGAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1800  
Qy 1801 CATACCCCTGCTTCAAGAAACCCAAAGACAGCTGCTCAGCGTTGACGTTGCTGTC 1860  
Db 1801 CATACCCCTGCTTCAAGAAACCCAAAGACAGCTGCTCAGCGTTGACGTTGCTGTC 1860  
Qy 1861 TCCTCCCTGGACATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1920  
Db 1861 TCCTCCCTGGACATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1920

Qy 1921 GTCACTCTGCACAGAGCCACAGACTCTCTCTGTCCTCCCTCATCTGCTCTTAAGATCAA 1980  
Db 1921 GTCACTCTGCACAGAGCCACAGACTCTCTCTGTCCTCCCTCATCTGCTCTTAAGATCAA 1980  
Qy 1981 CAGGTAAATCTCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2040  
Db 1981 CAGGTAAATCTCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2040  
Qy 2041 GAGCCCGGTCGCTCTTAAATTTCCCTTCTGACAGGAGTTCGAAACCACTACTCTCCAC 2100  
Db 2041 GAGCCCGGTCGCTCTTAAATTTCCCTTCTGACAGGAGTTCGAAACCACTACTCTCCAC 2100  
Qy 2101 ACATGAGAGGCGGTCGCTGAGCGTGGAGTCCCGGAGTCCCGGTTCACTGAGGAGCGGA 2160  
Db 2101 ACATGAGAGGCGGTCGCTGAGCGTGGAGTCCCGGAGTCCCGGTTCACTGAGGAGCGGA 2160  
Qy 2161 GACCTGTGACACAGAGCGCTGACAGATGAGAGTTCCTCCGTCGAGAGGTTGGTTG 2220  
Db 2161 GACCTGTGACACAGAGCGCTGACAGATGAGAGTTCCTCCGTCGAGAGGTTGGTTG 2220  
Qy 2221 AAATGCGGCGGCGAGCAAACTGACATGTTGAATGATAGCATTTCACTCTGCTGCTC 2280  
Db 2221 AAATGCGGCGGCGAGCAAACTGACATGTTGAATGATAGCATTTCACTCTGCTGCTC 2280  
Qy 2281 CTAGATCTGAGCAAGCTGTCTAGTTCTCACCCCGGAGTTCAGATGAGCTAACTTTT 2340  
Db 2281 CTAGATCTGAGCAAGCTGTCTAGTTCTCACCCCGGAGTTCAGATGAGCTAACTTTT 2340  
Qy 2341 TTAATGTCACAAAGCGCATCTCCAGATTCAGAGCCCTGCGCGCATGACTTTTCTGTA 2400  
Db 2341 TTAATGTCACAAAGCGCATCTCCAGATTCAGAGCCCTGCGCGCATGACTTTTCTGTA 2400  
Qy 2401 GGGTGTCTTCTCCCTGCTTCTGAGGTCGATAGAGCGAGTTCAGATGAGGAGTCC 2460  
Db 2401 GGGTGTCTTCTCCCTGCTTCTGAGGTCGATAGAGCGAGTTCAGATGAGGAGTCC 2460  
Qy 2461 TTAATGTCATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2520  
Db 2461 TTAATGTCATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2520  
Qy 2521 TGCAGGTCGCTGAGGTCATTTTGAAGTAGATATATTAACCTGCTTCTGCTATCTTCT 2580  
Db 2521 TGCAGGTCGCTGAGGTCATTTTGAAGTAGATATATTAACCTGCTTCTGCTATCTTCT 2580  
Qy 2581 GTCATTAATCTGCGGTACAGGTAATGAGATGTAAGTCTTCTTCTTCTTCTTCTTCTTCT 2640  
Db 2581 GTCATTAATCTGCGGTACAGGTAATGAGATGTAAGTCTTCTTCTTCTTCTTCTTCTTCT 2640  
Qy 2641 AGGATAAGCAAGACATTTTATACGATACCAAGTCACTATGCTGCTTCTTCTTCTTCTTCT 2700  
Db 2641 AGGATAAGCAAGACATTTTATACGATACCAAGTCACTATGCTGCTTCTTCTTCTTCTTCT 2700  
Qy 2701 AGGATTCGAAATTCATGAGTGCAGTATATTTTCTTAAAGTTTGGAAAGCAGGTTTTT 2760  
Db 2701 AGGATTCGAAATTCATGAGTGCAGTATATTTTCTTAAAGTTTGGAAAGCAGGTTTTT 2760  
Qy 2761 CTTTAAAGAAATTAAGACAGGTTCTCAATTAATTTAGTTCAGAAATTCCTAGACTGA 2820  
Db 2761 CTTTAAAGAAATTAAGACAGGTTCTCAATTAATTTAGTTCAGAAATTCCTAGACTGA 2820  
Qy 2821 AAGAACCTTAAACAAATAATTTTAAAGATATAAATATGCTGTATATGTTATGTAAT 2880  
Db 2821 AAGAACCTTAAACAAATAATTTTAAAGATATAAATATGCTGTATATGTTATGTAAT 2880  
Qy 2881 TTATTTTGGCTTAAATACATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2940  
Db 2881 TTATTTTGGCTTAAATACATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2940  
Qy 2941 AAAAA 2945  
Db 2941 AAAAA 2945



RESULT 6  
 ACAT71627  
 ACAT71627 standard; cDNA; 2945 BP.  
 ACAT71627;  
 11-AUG-2003 (first entry)  
 Human secreted and transmembrane polypeptide PRO274 cDNA.  
 Human; ss; gene; thrombolytic agent; interferon; interleukin; cytokine;  
 erythropoietin; colony stimulating factor; cancer; colorectal carcinoma;  
 apoptosis related condition; AIDS; amyotrophic lateral sclerosis;  
 inflammatory disease; asthma; atherosclerosis; neurodegenerative disease;  
 gastrointestinal disorder; Alzheimer's disease; Parkinson's disease;  
 hypertension; myocardial ischemia; kidney disease; carcinogenesis;  
 glomerulonephritis; lung disease; pulmonary hypertension; preclampsia;  
 bronchial asthma; gastric ulcer; renal failure; cardiovascular disease;  
 inflammatory bowel disease; reproductive disorder; premature labour.  
 Homo sapiens. OS XX  
 US2002177553-Al. EN  
 28-NOV-2002. XX  
 15-OCT-2001; 2001US-00978192. PF  
 17-OCT-1997; 97US-0062250P. PP  
 03-NOV-1997; 97US-0064249P. PR  
 13-NOV-1997; 97US-0065311P. PR  
 21-NOV-1997; 97US-0065364P. PR  
 10-MAR-1998; 98US-0077450P. PR  
 11-MAR-1998; 98US-0077632P. PR  
 11-MAR-1998; 98US-0077641P. PR  
 12-MAR-1998; 98US-0077791P. PR  
 13-MAR-1998; 98US-0078004P. PR  
 17-MAR-1998; 98US-0080422P. PR  
 20-MAR-1998; 98US-0078886P. PR  
 20-MAR-1998; 98US-0078910P. PR  
 20-MAR-1998; 98US-0078936P. PR  
 20-MAR-1998; 98US-0078939P. PR  
 25-MAR-1998; 98US-0079294P. PR  
 26-MAR-1998; 98US-0079556P. PR  
 27-MAR-1998; 98US-0079663P. PR  
 27-MAR-1998; 98US-0079664P. PR  
 27-MAR-1998; 98US-0079689P. PR  
 27-MAR-1998; 98US-0079728P. PR  
 27-MAR-1998; 98US-0079786P. PR  
 30-MAR-1998; 98US-0079820P. PR  
 30-MAR-1998; 98US-0079823P. PR  
 26-JUN-1998; 98US-00105413. PR  
 07-OCT-1998; 98US-00168978. PR  
 07-OCT-1998; 98US-0021141. PR  
 02-NOV-1998; 98US-00184216. PR  
 06-NOV-1998; 98US-00187368. PR  
 20-NOV-1998; 98US-0024855. PR  
 07-DEC-1998; 98US-00202054. PR  
 22-DEC-1998; 98US-00218517. PR  
 05-JAN-1999; 99WO-US000106. PR  
 05-MAR-1999; 99US-00254465. PR  
 08-MAR-1999; 99WO-US0005028. PR  
 10-MAR-1999; 99US-00265686. PR  
 10-MAR-1999; 99WO-US0005190. PR  
 12-MAR-1999; 99US-00267213. PR  
 12-APR-1999; 99US-00284291. PR  
 14-MAY-1999; 99US-00311832. PR  
 14-MAY-1999; 99WO-US010733. PR  
 02-JUN-1999; 99WO-US012252. PR  
 25-AUG-1999; 99US-00380137. PR

CC	amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,	
CC	atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,	
CC	Parkinson's disease; cardiovascular disease e.g. hypertension and	
CC	myocardial ischemia; kidney disease e.g. renal failure and	
CC	glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial	
CC	asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory	
CC	bowel disease; reproductive disorders e.g. premature labour and	
CC	pre-eclampsia; carcinogenesis. The present sequence represents a cDNA	
CC	encoding a PRO polypeptide of the invention. Note: The sequence data for	
CC	this patent did not form part of the printed specification but was	
CC	obtained in electronic format directly from USPTO at	
CC	seqdata.uspto.gov/sequence.html?DocID=20020177553	
XX		
SQ	Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 2945; DB 7; Length 2945;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CGCTCGCCCGTGGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTTGTG 60	
DB	1 CGCTCGCCCGTGGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTTGTG 60	
QY	61 GGGTCAGCCACGCGGGGAGCTATGGTGAATTCGCGCGCTCAGCAGTACTGCGCCCT 120	
DB	61 GGGTCAGCCACGCGGGGAGCTATGGTGAATTCGCGCGCTCAGCAGTACTGCGCCCT 120	
QY	121 GATCCGGTCTTGGTGGCCCTGGGCATCACCAATAGCATCGACTTCGGGGAGCAGG 180	
DB	121 GATCCGGTCTTGGTGGCCCTGGGCATCACCAATAGCATCGACTTCGGGGAGCAGG 180	
QY	181 CTTGAACCGGGGCAATGCTGCTGTCAAGGAGGATGAGTCGAGATGCTGGCCAGTACGG 240	
DB	181 CTTGAACCGGGGCAATGCTGCTGTCAAGGAGGATGAGTCGAGATGCTGGCCAGTACGG 240	
QY	241 GCTGGGTAATCCCTCATGAACTTCTCACGGGTCCCATGAGTACTCAAAATGTTGGG 300	
DB	241 GCTGGGTAATCCCTCATGAACTTCTCACGGGTCCCATGAGTACTCAAAATGTTGGG 300	
QY	301 CTTGGTGTGTTGTAACAGCAAGAGAGACAGGACCAAGCCGCTCTGTATGTTGGTGGC 360	
DB	301 CTTGGTGTGTTGTAACAGCAAGAGAGACAGGACCAAGCCGCTCTGTATGTTGGTGGC 360	
QY	361 AGGGGCATCGCTGCGCTTTTCAACACTGATGATCTATAGTATGATGATGATGATGAT 420	
DB	361 AGGGGCATCGCTGCGCTTTTCAACACTGATGATCTATAGTATGATGATGATGATGAT 420	
QY	421 TATCAATAAATCGCACTGTCGAGTGGAGTGGGTCGAGCAAGACGAGAGGCGCTTCT 480	
DB	421 TATCAATAAATCGCACTGTCGAGTGGAGTGGGTCGAGCAAGACGAGAGGCGCTTCT 480	
QY	481 GTACCTCGCCGCTTTTCTTTCATGGAACGCAATGGGATGGACCCATGCTGGCATTTCT 540	
DB	481 GTACCTCGCCGCTTTTCTTTCATGGAACGCAATGGGATGGACCCATGCTGGCATTTCT 540	
QY	541 AAAACAAATACAGTTTCTCGTGGGATGGCTCAATCTCAGATGTCATAGCTCAGGT 600	
DB	541 AAAACAAATACAGTTTCTCGTGGGATGGCTCAATCTCAGATGTCATAGCTCAGGT 600	
QY	601 TGTGTTTGTAGCAATTTCTTTCACAGTCACTGGAATGCCGGAGCCCTGCTCATCCC 660	
DB	601 TGTGTTTGTAGCAATTTCTTTCACAGTCACTGGAATGCCGGAGCCCTGCTCATCCC 660	
QY	661 GATCTCTCTCTGTACATGGGGCACTTGTGGCTGCGACCCATGCTGGGCTACTA 720	
DB	661 GATCTCTCTCTGTACATGGGGCACTTGTGGCTGCGACCCATGCTGGGCTACTA 720	
QY	721 CAAGAAATTCAGCAATCATCCCTGACAGAGTGGCCCGGAGCTGGGGAGATGCAAC 780	
DB	721 CAAGAAATTCAGCAATCATCCCTGACAGAGTGGCCCGGAGCTGGGGAGATGCAAC 780	
QY	781 AATAAGAAATGCTGAGCTTTCTGGTGGCTTTGGCTCTAATCTGGGCCACACAGAAAT 840	

DB	781 AATAAGAAATGCTGAGCTTCTGGTGGCTTTGGCTCTAATCTGGGCCACACAGAAAT 840	
QY	841 CAGTGGCCCTATTGTCAACCTCTTTGTTTCCCGGACCTTGTGGCAGTTCTGACGCCAC 900	
DB	841 CAGTGGCCCTATTGTCAACCTCTTTGTTTCCCGGACCTTGTGGCAGTTCTGACGCCAC 900	
QY	901 AGAGGAGTGGCGATTTTACAGCCACATACCTTGGTTCACATGCCATGCGGTGTT 960	
DB	901 AGAGGAGTGGCGATTTTACAGCCACATACCTTGGTTCACATGCCATGCGGTGTT 960	
QY	961 GACGGAATCCGTTGTTGTATCTCTGCTTTCACAGAAATTAACCCAGCAACAACTGTT 1020	
DB	961 GACGGAATCCGTTGTTGTATCTCTGCTTTCACAGAAATTAACCCAGCAACAACTGTT 1020	
QY	1021 GAGCAGAGCAACACAGTCAAGGAGCCACATCAAGAGTTTCACTTCTGTCATGGC 1080	
DB	1021 GAGCAGAGCAACACAGTCAAGGAGCCACATCAAGAGTTTCACTTCTGTCATGGC 1080	
QY	1081 TCTGTCACTCAAGCTCTGTTGTTGTTTGGACACCCAACTGTTCTGAGAAATCTT 1140	
DB	1081 TCTGTCACTCAAGCTCTGTTGTTGTTTGGACACCCAACTGTTCTGAGAAATCTT 1140	
QY	1141 GATAGACATCAAGTGGAGCTTTCCTTTCAGAACTCTGTGTTGTTCTTTCGGGAT 1200	
DB	1141 GATAGACATCAAGTGGAGCTTTCCTTTCAGAACTCTGTGTTGTTCTTTCGGGAT 1200	
QY	1201 CTTCTCTCTTCTCCAGTTCCAGTCAAGTGGGCGCATCTCACCGGTGCTCATGAC 1260	
DB	1201 CTTCTCTCTTCTCCAGTTCCAGTCAAGTGGGCGCATCTCACCGGTGCTCATGAC 1260	
QY	1261 ACTGAAGAAAACCTTCTGCTTTCGCTTTCGCTGCGGATCATGCTCTCATCGC 1320	
DB	1261 ACTGAAGAAAACCTTCTGCTTTCGCTTTCGCTGCGGATCATGCTCTCATCGC 1320	
QY	1321 CAGCTCTGCTGCTTCTTCTTCTGCTGCGGAGTGGGCGGAGCTCTGCGGCTGCTTCT 1380	
DB	1321 CAGCTCTGCTGCTTCTTCTTCTGCTGCGGAGTGGGCGGAGCTCTGCGGCTGCTTCT 1380	
QY	1381 CTTGGGCGGCTTGTGGGAGATCCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440	
DB	1381 CTTGGGCGGCTTGTGGGAGATCCACCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440	
QY	1441 GAAGCAGAAAAGAGATGAGTGGGAGTGGGCGGAGGAGGAGCTCTGCGCATGAC 1500	
DB	1441 GAAGCAGAAAAGAGATGAGTGGGAGTGGGCGGAGGAGGAGCTCTGCGCATGAC 1500	
QY	1501 AGACATGCTCTCCGACAGAGAGGTGACAGATCGTGGAAATGAGAGAGAGATGAATA 1560	
DB	1501 AGACATGCTCTCCGACAGAGAGGTGACAGATCGTGGAAATGAGAGAGAGATGAATA 1560	
QY	1561 AGGACGGGACGCGCATGGGACCTGACGAGGAGGAGTGGGAGGAGCTCTGCGCATCAT 1620	
DB	1561 AGGACGGGACGCGCATGGGACCTGACGAGGAGGAGTGGGAGGAGCTCTGCGCATCAT 1620	
QY	1621 CTCTTCTCTCTCCCATGATTTTGTTCCTTTTGTTCCTTTTGTTCCTTTTGTTCCTTT 1680	
DB	1621 CTCTTCTCTCTCCCATGATTTTGTTCCTTTTGTTCCTTTTGTTCCTTTTGTTCCTTT 1680	
QY	1681 GGGCTTGAATTAAGGTTTGGTCAATTTCTTAGCATGCTGCTGCTGCTGCTGCTGCTG 1740	
DB	1681 GGGCTTGAATTAAGGTTTGGTCAATTTCTTAGCATGCTGCTGCTGCTGCTGCTGCTG 1740	
QY	1741 GGGGACCTAGTGAATGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1800	
DB	1741 GGGGACCTAGTGAATGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1800	
QY	1801 CATACCCCTGCTCAGAAAACCCAAAGACACAGCTGCTCAGGTTGAGCTGTTGTTCC 1860	
DB	1801 CATACCCCTGCTCAGAAAACCCAAAGACACAGCTGCTCAGGTTGAGCTGTTGTTCC 1860	
QY	1861 TCTCTCCCTGAGCAATCTCTCTTGGAAACCAAGGAGTGGAGCTGCTGCTGCTGCTG 1920	
DB	1861 TCTCTCCCTGAGCAATCTCTCTTGGAAACCAAGGAGTGGAGCTGCTGCTGCTGCTG 1920	









polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, sarcoma, leukemia or lymphoma), inflammatory disease, necrosis, atherosclerosis, infertility, premature aging, psoriasis, inflammation, arthritis, multiple sclerosis in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence encodes a PRO polypeptide

Sequence 2945 BP; 703 A; 776 C; 705 G; 761 T; 0 U; 0 Other;

Query Match 100.0%; Score 2945; DB 7; Length 2945;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTCGCCCGTCGCGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60  
DB 1 CGCTCGCCCGTCGCGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60

QY 61 GGGTCAGCCCAAGCGGGGACTATGGTGAATTCGCCGGCTCAGCACTACTGCCCCCT 120  
DB 61 GGGTCAGCCCAAGCGGGGACTATGGTGAATTCGCCGGCTCAGCACTACTGCCCCCT 120

QY 121 GATCGCGTCTTGTGTCCTCGGCTCAGCAATACCAATAGCATCGACTTCGGGGAGCAGGC 180  
DB 121 GATCGCGTCTTGTGTCCTCGGCTCAGCAATACCAATAGCATCGACTTCGGGGAGCAGGC 180

QY 181 CTTGAACCGGGCAATGTCTGTCAAGAGAGATGAGTGTGAGTGTGCTGGCAGTACGG 240  
DB 181 CTTGAACCGGGCAATGTCTGTCAAGAGAGATGAGTGTGAGTGTGCTGGCAGTACGG 240

QY 241 GCTGGCGTACTCCCTCATGAGTCTTCCAGGGTCCCATGAGTGAATTCAGAAATGTGGG 300  
DB 241 GCTGGCGTACTCCCTCATGAGTCTTCCAGGGTCCCATGAGTGAATTCAGAAATGTGGG 300

QY 301 CTTGTGTGTTGTGAACAGCAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGC 360  
DB 301 CTTGTGTGTTGTGAACAGCAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGC 360

QY 361 AGGGGCATCGTCCGCTCTTTCACACTGATGATGATGATGATGATGATGATGATGAT 420  
DB 361 AGGGGCATCGTCCGCTCTTTCACACTGATGATGATGATGATGATGATGATGATGAT 420

QY 421 TATCAATAAATGCAACATGTGACGAGTCCGTGGGGAGCAAGAGAGAGAGAGAGAGAG 480  
DB 421 TATCAATAAATGCAACATGTGACGAGTCCGTGGGGAGCAAGAGAGAGAGAGAGAGAG 480

QY 481 GTACCTCGCCGCTTCTCTTTCATGAGCAGATGAGCAGATGAGCAGATGAGCAGATGAG 540  
DB 481 GTACCTCGCCGCTTCTCTTTCATGAGCAGATGAGCAGATGAGCAGATGAGCAGATGAG 540

QY 541 ABAACACAATACAGTTCTCTGTGGATGTGCTCAATCTCAGATGTCTAGCTCAGGT 600  
DB 541 ABAACACAATACAGTTCTCTGTGGATGTGCTCAATCTCAGATGTCTAGCTCAGGT 600

QY 601 TGTGTTGTAGCCATTTGCTTCAAGTCACTGGAAATGCGGGAGCCCTGCTATGCC 660  
DB 601 TGTGTTGTAGCCATTTGCTTCAAGTCACTGGAAATGCGGGAGCCCTGCTATGCC 660

QY 661 GATCCTCTCTGTACATGGGCGACTTGTGCGCTGCACACCGCTGCTGGGCTACTA 720  
DB 661 GATCCTCTCTGTACATGGGCGACTTGTGCGCTGCACACCGCTGCTGGGCTACTA 720

QY 721 CAAGAACATTCAGACATCATCCTGTACAGAGTGGCCCGAGCTGGGGGAGATGCAAC 780  
DB 721 CAAGAACATTCAGACATCATCCTGTACAGAGTGGCCCGAGCTGGGGGAGATGCAAC 780

QY 781 AATAAGAAAGATGCTGAGCTTCTGTGGCTTGGCTCTAATTCGGCCACACAGAGAT 840  
DB 781 AATAAGAAAGATGCTGAGCTTCTGTGGCTTGGCTCTAATTCGGCCACACAGAGAT 840

QY 841 CAGTCGGCTATGTCAACCTCTTTTCCGGGACCTTGGTGGCAGTTCTGACGCCAC 900  
DB 841 CAGTCGGCTATGTCAACCTCTTTTCCGGGACCTTGGTGGCAGTTCTGACGCCAC 900

QY 901 AGAGGAGTGGGATTTTTCAGAGCACAATACCTGTGGGTCACTAGCCATGCGTGT 960  
DB 901 AGAGGAGTGGGATTTTTCAGAGCACAATACCTGTGGGTCACTAGCCATGCGTGT 960

QY 961 GAGGGAATCCGTGCTGTATCTCTTCCAGAGATAACCCAGCAACAACTGCT 1020  
DB 961 GAGGGAATCCGTGCTGTATCTCTTCCAGAGATAACCCAGCAACAACTGCT 1020

QY 1021 GAGCAGAGCAACACAGTCAAGGAGCCCACTCAAGAAAGTTCACTTCTGTGATGGC 1080  
DB 1021 GAGCAGAGCAACACAGTCAAGGAGCCCACTCAAGAAAGTTCACTTCTGTGATGGC 1080

QY 1081 TCTGTCACTCAGCTCTGTGTTTGGTGTATGTTTGGACACCAACGTTCTGAGAAATCT 1140  
DB 1081 TCTGTCACTCAGCTCTGTGTTTGGTGTATGTTTGGACACCAACGTTCTGAGAAATCT 1140

QY 1141 GATAGACATCATCGAGTGGACTTTGCCCTTGCAGAACTCTGTGTTTCTTTCGGAT 1200  
DB 1141 GATAGACATCATCGAGTGGACTTTGCCCTTGCAGAACTCTGTGTTTCTTTCGGAT 1200

QY 1201 CTTCTCTTCTCCAGTTCCAGTCAAGTGGGGGCACTCTCACGGGTGGGTGATGAC 1260  
DB 1201 CTTCTCTTCTCCAGTTCCAGTCAAGTGGGGGCACTCTCACGGGTGGGTGATGAC 1260

QY 1261 ACTGAAGAAACCTTCTGCTTCCCTCCAGCTCTGTGCTGCGGATCATGCTCTCATCGC 1320  
DB 1261 ACTGAAGAAACCTTCTGCTTCCCTCCAGCTCTGTGCTGCGGATCATGCTCTCATCGC 1320

QY 1321 CAGCTCTGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380  
DB 1321 CAGCTCTGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380

QY 1381 CTTGCGGGCTTGTGGGAGAAATCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
DB 1381 CTTGCGGGCTTGTGGGAGAAATCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440

QY 1441 GAAGCAGAAAAAGATGGAGAAATGAGTCGGCCACGAGGGGGAAGACTCTGCCATGAC 1500  
DB 1441 GAAGCAGAAAAAGATGGAGAAATGAGTCGGCCACGAGGGGGAAGACTCTGCCATGAC 1500

QY 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGATGAATA 1560  
DB 1501 AGACATGCTCCGACAGAGAGGTGACAGACATCGTGGAAATGAGAGAGAGATGAATA 1560

QY 1561 AGGCACGGGACCCATGCGGACCTGCGAGGACGGTCACTCAGGATGACACTTCGGCATCAT 1620  
DB 1561 AGGCACGGGACCCATGCGGACCTGCGAGGACGGTCACTCAGGATGACACTTCGGCATCAT 1620

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Db 2941 AAAAA 2945  
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XX  
DT 20-NOV-2003 (first entry)  
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XX  
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chromosome identification; vaccine; cancer; retinal disorder;  
wound healing; obesity; diabetes; hearing loss;  
cardiac insufficiency disorder; kidney disorder; nervous system disorder;  
haemoglobin associated disorder.  
XX  
OS Homo sapiens.  
XX  
PN US2003050241-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 16-OCT-2001; 2001US-00978564.  
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PR 03-NOV-1997; 97US-0064249P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 21-NOV-1997; 97US-0066364P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
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PR 12-MAR-1998; 98US-0077649P.  
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PR 20-MAR-1998; 98US-0078866P.  
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PR 30-MAR-1998; 98US-0079920P.  
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PR 08-APR-1998; 98US-0081049P.  
PR 08-APR-1998; 98US-0081070P.  
PR 08-APR-1998; 98US-0081071P.  
PR 09-APR-1998; 98US-0081195P.  
PR 09-APR-1998; 98US-0081203P.  
PR 09-APR-1998; 98US-0081229P.  
PR 15-APR-1998; 98US-0081817P.  
PR 15-APR-1998; 98US-0081819P.  
PR 15-APR-1998; 98US-0081838P.  
PR 15-APR-1998; 98US-0081952P.  
PR 15-APR-1998; 98US-0081955P.  
PR 21-APR-1998; 98US-0082568P.  
PR 21-APR-1998; 98US-0082569P.



PR	22-APR-1998;	98US-0082700P.	PR	30-NOV-1999;	99WO-US028313.	PR	30-NOV-1999;	99WO-US028313.
PR	22-APR-1998;	98US-0082704P.	PR	02-DEC-1999;	99WO-US028551.	PR	02-DEC-1999;	99WO-US028551.
PR	22-APR-1998;	98US-0082797P.	PR	16-DEC-1999;	99WO-US030095.	PR	16-DEC-1999;	99WO-US030095.
PR	22-APR-1998;	98US-0082804P.	PR	30-DEC-1999;	99WO-US031243.	PR	30-DEC-1999;	99WO-US031243.
PR	27-APR-1998;	98US-0083336P.	PR	05-JAN-2000;	2000WO-US000219.	PR	05-JAN-2000;	2000WO-US000219.
PR	27-APR-1998;	98US-0083332P.	PR	06-JAN-2000;	2000WO-US000277.	PR	06-JAN-2000;	2000WO-US000277.
PR	28-APR-1998;	98US-0083332P.	PR	11-FEB-2000;	2000WO-US003376.	PR	11-FEB-2000;	2000WO-US003376.
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PR	29-APR-1998;	98US-0083559P.	PR	22-MAY-2000;	2000WO-US014042.	PR	22-MAY-2000;	2000WO-US014042.
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PR	05-MAY-1998;	98US-0084366P.	PR	02-JUN-2000;	2000WO-US015264.	PR	02-JUN-2000;	2000WO-US015264.
PR	06-MAY-1998;	98US-0084414P.	PR	28-JUL-2000;	2000WO-US020710.	PR	28-JUL-2000;	2000WO-US020710.
PR	06-MAY-1998;	98US-0084414P.	PR	24-AUG-2000;	2000WO-US023328.	PR	24-AUG-2000;	2000WO-US023328.
PR	07-MAY-1998;	98US-0084598P.	PR	01-DEC-2000;	2000WO-US034956.	PR	01-DEC-2000;	2000WO-US034956.
PR	07-MAY-1998;	98US-0084600P.	PR	28-FEB-2001;	2001WO-US0006520.	PR	28-FEB-2001;	2001WO-US0006520.
PR	07-MAY-1998;	98US-0084637P.	PR	22-MAR-2001;	2001WO-US0009552.	PR	22-MAR-2001;	2001WO-US0009552.
PR	07-MAY-1998;	98US-0084640P.	PR	23-MAY-2001;	2001WO-US017092.	PR	23-MAY-2001;	2001WO-US017092.
PR	07-MAY-1998;	98US-0084643P.	PR	01-JUN-2001;	2001WO-US017800.	PR	01-JUN-2001;	2001WO-US017800.
PR	13-MAY-1998;	98US-0085323P.	PR	20-JUN-2001;	2001WO-US019692.	PR	20-JUN-2001;	2001WO-US019692.
PR	13-MAY-1998;	98US-0085338P.	PR	29-JUN-2001;	2001WO-US021066.	PR	29-JUN-2001;	2001WO-US021066.
PR	13-MAY-1998;	98US-0085339P.	PR	09-JUL-2001;	2001WO-US021735.	PR	09-JUL-2001;	2001WO-US021735.
PR	15-MAY-1998;	98US-0085573P.	PR	30-JUL-2001;	2001US-00918585.	PR	30-JUL-2001;	2001US-00918585.
PR	15-MAY-1998;	98US-0085573P.	XX			XX		
PR	15-MAY-1998;	98US-0085580P.	PA	(GETH ) GENENTECH INC.		PA		
PR	15-MAY-1998;	98US-0085582P.	XX			XX		
PR	15-MAY-1998;	98US-0085689P.	PI	Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		PI		
PR	15-MAY-1998;	98US-0085697P.	PI	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;		PI		
PR	15-MAY-1998;	98US-0085700P.	PI	Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;		PI		
PR	15-MAY-1998;	98US-0085704P.	PI	Klavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;		PI		
PR	18-MAY-1998;	98US-0086023P.	PI	Stewart TA, Tumas D, Williams PM, Wood WI;		PI		
PR	22-MAY-1998;	98US-0086392P.	XX			XX		
PR	22-MAY-1998;	98US-0086414P.	DR	WPI; 2003-521814/49.		DR		
PR	22-MAY-1998;	98US-0086430P.	DR	P-PSDB; ADA24546.		DR		
PR	22-MAY-1998;	98US-0086486P.	XX			XX		
PR	28-MAY-1998;	98US-0087098P.	PT	New isolated PRO polypeptides for example extracellular, secreted and		PT		
PR	28-MAY-1998;	98US-0087106P.	PT	membrane bound proteins, useful for modulating the biological activities		PT		
PR	28-MAY-1998;	98US-0087208P.	PT	of cells and for treating, for example diabetes, cancer, rheumatoid		PT		
PR	26-JUN-1998;	98US-0090863P.	PT	arthritis, and hearing loss.		PT		
PR	01-JUL-1998;	98US-0091359P.	XX	Claim 2; Fig 3; 461pp; English.		XX		
PR	11-SEP-1998;	98US-0100038P.	XX			XX		
PR	07-OCT-1998;	98WO-US021141.	CC	The invention describes an isolated secreted and transmembrane (PRO)		CC		
PR	20-NOV-1998;	98US-0109304P.	CC	polypeptide (I). PRO337 polypeptide is useful for detecting PRO4993		CC		
PR	20-NOV-1998;	98WO-US024855.	CC	polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are		CC		
PR	22-DEC-1998;	98US-0113296P.	CC	useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is		CC		
PR	23-DEC-1998;	98US-0113621P.	CC	useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO4993 is		CC		
PR	03-JAN-1999;	99WO-US000106.	CC	useful for linking a bioactive molecule to a cell expressing a PRO337		CC		
PR	08-MAR-1999;	99WO-US005028.	CC	polypeptide, and PRO337 is useful for linking a bioactive molecule to a		CC		
PR	10-MAR-1999;	99WO-US005190.	CC	cell expressing a PRO4993 polypeptide. PRO1559 is useful for linking a		CC		
PR	12-MAR-1999;	99US-0123957P.	CC	bioactive molecule to a cell expressing a PRO735, PRO700 and PRO739		CC		
PR	21-APR-1999;	99US-0126773P.		Query Match 100.0%; Score 2945; DB 8; Length 2945;				
PR	26-APR-1999;	99US-0130232P.		Best Local Similarity 100.0%; Pred. No. 0;				
PR	26-APR-1999;	99US-0131022P.		Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
PR	14-MAY-1999;	99US-0134287P.	QY	1 CGCTCGCCCCCTCGCCCCCTCGCCCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60				
PR	14-MAY-1999;	99WO-US010733.	Db	1 CGCTCGCCCCCTCGCCCCCTCGCCCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTG 60				
PR	02-JUN-1999;	99US-0139557P.	QY	61 GGGTCAGCCACGGCGGGGACTATGGTGAATTCGGCGGCTCAGCAGTCTGCCCCCT 120				
PR	16-JUN-1999;	99US-0141037P.	Db	61 GGGTCAGCCACGGCGGGGACTATGGTGAATTCGGCGGCTCAGCAGTCTGCCCCCT 120				
PR	07-JUL-1999;	99US-0142680P.						
PR	26-JUL-1999;	99US-0145698P.						
PR	28-JUL-1999;	99US-0146222P.						
PR	29-OCT-1999;	99US-0162506P.						

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QY 301 CTTGGTCTTTGTGAACAGCAGAGAGACAGCAACAAAGCCGTCTCTGTATGTGTGG 360  
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PR 13-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
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PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US0005028.
PR 10-MAR-1999; 99WO-US0005190.
PR 12-MAR-1999; 99US-0123957P.
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PR 21-APR-1999; 99US-0130232P.
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PR 30-OCT-1999; 99US-0162506P.
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PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
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PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US003565.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
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PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
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PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
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PR PA (GETH ) GENENTECH INC.
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PR PI Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
PR PI Perrara N, Filvaroff E, Pong S, Gao W, Gerber H, Gerritsen MB;
PR PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PR PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoi NF, Roy MA, Shelton DL;
PR PI Stewart TA, Tumas D, Williams PM, Wood WL;
XX
PR DR WPI; 2003-503575/47.
PR DR P-PSDB; ABO19643.
XX
PR XX Novel secreted and transmembrane polypeptide for modulating biological
PR PT activity of cell expressing the polypeptide, identifying agonists or
PR PT antagonists of polypeptide, and as molecular weight markers.
XX
PR PS Claim 2; Fig 3; 459pp; English.
XX
PR CC The invention describes an isolated, secreted and transmembrane
PR CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
PR CC PRO4993, PRO337, PRO1599, PRO725, PRO700 or PRO739 polypeptide, and for
PR CC linking a bioactive molecule to a cell expressing the above polypeptides.
PR CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
PR CC cell death. (I) is useful as therapeutic agent, in medical and industrial
PR CC applications e.g. for treating neuropathy, especially peripheral
PR CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
PR CC Charcot-Marie-Tooth disease, Refsum's disease, Abetalipoproteinaemia,
PR CC

Query Match 100.0%; Score 2945; DB 8; Length 2945;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 GATCGGTTCTGTGTCCTCGCCCTGGGCATCCCAACATAGCCATCGACTTCGGGGAGCAGC 180
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PR 05-JAN-1999; 99WO-US000106.
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PR 08-MAR-1999; 99WO-US0005038.
PR 10-MAR-1999; 99US-000865686.
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PR 08-NOV-2000; 2000US-00709238.
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PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH ) GENENTECH INC.
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XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Paton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KW sport-related joint problem; articular cartilage defect; osteoarthritis;  
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;  
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;  
KW celiac disease; dermatitis; Crohn disease; neuropathy;  
KW cardiac insufficiency disorder; peripheral neuropathy;  
KW diabetic peripheral neuropathy; autonomic neuropathy;  
KW reduced motility of the gastrointestinal tract;  
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;  
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;  
KW Refsum's disease; Gene; ss.

XX Homo sapiens.

XX US2003049633-A1.

XX 13-MAR-2003.

XX 16-OCT-2001; 2001US-00978585.

XX 17-OCT-1997; 97US-0062250P.

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PR 27-APR-1998; 98US-0083336P.

PR	28-APR-1998	98US-0083322P.	PR	05-JAN-2000	200WO-US000219.	XX	(GETH ) GENENTECH INC.	PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME; Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ; Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL; Stewart TA, Tumas D, Williams PM, Wood WI;
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PR	29-APR-1998	98US-0083495P.	PR	06-JAN-2000	200WO-US000376.	DR	P-PSDB; ADB76229.	DR	New PRO polypeptides useful for treating peripheral neuropathy, neuropathies associated with systemic disease such as post-polio syndrome or AIDS-associated syndrome.
PR	29-APR-1998	98US-0083496P.	PR	11-FEB-2000	200WO-US003565.	XX		PT	Claim 2; Fig 3; 425pp; English.
PR	29-APR-1998	98US-0083499P.	PR	18-FEB-2000	200WO-US004341.	CC		CC	The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The bioactive molecule maybe a toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides are useful for treating neuropathy and neuropathy related diseases such as Charcot-Marie-Tooth disorder, Refsum's disease, and Krabbe's disease. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation
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KW sports-related joint problem; articular cartilage defects;
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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c 20	1491.6	50.6	142056	9	AC010491	Homo sapi
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22	1435.8	48.8	2593	10	AF274752	Mus muscu
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24	1244.2	42.2	2405	10	MMFN5452	Mus muscu
25	1102.4	37.4	1721	6	AX877570	Sequence
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c 37	326.6	11.1	356	11	G25711	human STS E
38	317	10.8	357	10	MMFN5451	Mus muscu
c 39	220.8	7.5	130052	2	AC022496	Homo sapi
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ALIGNMENTS

RESULT 1  
AX201336  
LOCUS AX201336 2945 bp DNA linear PAT 30-AUG-2001  
DEFINITION Sequence 15 from Patent WO0153486.  
ACCESSION AX201336  
VERSION AX201336.1 GI:15391161  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V.,  
Stone, D.M., Watanabe, C.K. and Wood, W.I.

TITLE Compositions and methods for the treatment of tumour  
JOURNAL Patent: WO 0153486-A 15 26-JUL-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 2945; DB 6; Length 2945;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AY358503  
VERSION AY358503.1 GI:37182128  
KEYWORDS FLI CDNA  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 2945)  
AUTHORS Clark,H.P., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagstad,A., Vandlen,R., Watanabe,C., Wieand,B., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.  
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment  
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 2945)  
AUTHORS Clark,H.P.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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LOCUS Homo sapiens mRNA for KIAA1581 protein, partial cds.
DEFINITION AB046801
ACCESSION AB046801
VERSION AB046801.1 GI:10047236
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Nagase,T., Kikuno,R., Nakayama,M., Hirose,M. and Ohara,O.
Prediction of the coding sequences of unidentified human genes.
XVII. The complete sequences of 100 new cDNA clones from brain
which code for large proteins in vitro
DNA Res. 7 (4), 273-281 (2000)
JOURNAL MEDLINE
PUBMED 20450683
REFERENCE 10997877
AUTHORS 2 (bases 1 to 328)
TITLE Chara,O., Nagase,T. and Kikuno,R.
JOURNAL Direct Submission
Submitted (03-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdna@kazusa.or.jp),
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
Fax:81-438-52-3914)
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2939; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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[illegible]

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QY	2215	GGTTGGAAATGCCCGGGGGCAGCAAACTGACATGGTTGAATGATAGCAATTTTCACTCTGC	2274
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QY	2275	GTTCCTCTAGATCTGAGCAAGCTGTGAGTTCTCACCCGCCACCCGTGTATATACATGAGCTA	2334
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DB	1999	GCATCTCAACTTTTGCAATTTTAGTTTTACAGTGAACGTAAAGCTTTAAGTCTCATCCAGCA	1958
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## RESULT 7

RESOL 7  
AK130676

LOCUS

## DEFINITION

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ACCESSION

**VERSION**

## KEYWORDS

**SOURCE**

## ORGANI

AK130676 2152 bp mRNA linear PRI 10-SEP-2003  
Homo sapiens cDNA FLJ27166 fis, clone SYN01530, highly similar to  
Homo sapiens progressive ankylosis-like protein (ANK) mRNA.

НОВО ВАРПЕНА ПРОГРЕСИВНО АНУЛОВНО-ТИП ПРОСВЕТА (1940-1944)  
AK130676

AK130676  
AK130676.1 GI:34527530

AK130676.1 GI:3427250  
oligo capping; fis (full insert sequence).

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

[illegible]

Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S.,

Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,  
Watanabe, Y., Mizuno, S., Morinaga, M.

Suzuki, Y.,	Hata, H.,	Nakagawa, K.,	Mizuno, S.,	Morinaga, M.,
Takahashi, M.	Ogura, T.	Iwano, B.	Otsuki, T.	Sato, H.

Kawamura, M., Sugiyama, T., Irie, K., Otsuki, T., Sato, H.,  
Nishikawa T. Sugiyama T. Kawakami B. Nagai K. Isogai, T. and

Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, I. and Sugano S

Sugano, S.



TITLE		NEDO human cDNA sequencing project	
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 2152)		
AUTHORS	Sugano,S. and Suzuki,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-JUL-2003)		
University of Tokyo, Laboratory of Genome Science, Institute of Medical Science, Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)			
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing: RAB; clone selection for full insert sequencing: RAB and Helix Research Institute.			
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Matches 2150; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
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Location/Qualifiers

Location/Qualifiers

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57.5%; Score 1692.4; DB 9; Length 1892;  
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 Cons. 93.3; Conservative 1; Indels 0; Gaps 0

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295	GATCCGGTCTTTGGTGGCCCTGGGCATCACCAATAGCCATCGACTTCGGGGACGAGC	354
181	CTTGAAACGGGGCATTTGCTGTCTGTCAGGAGGATGCAGTCTGGCCAGCTACGG	240
355	CTTGAAACGGGGCATTTGCTGTCTGTCAGGAGGATGCAGTCTGGCCAGCTACGG	414
441	GCTGGCGTACTCCCTCATGAAGTTCCTTCACGGGTCCCATGAGTGCATCTCAAAAATGTGGG	300

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cDNA Library Preparation: ResGen, Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: nisc.mcgenhri.nih.gov

Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dierich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P.,  
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McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 116 Row: g Column: 21  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 9994166.

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ORIGIN

Query Match 53.8%; Score 1585.2; DB 10; Length 3468;  
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Matches 2295; Conservative 0; Mismatches 468; Indels 189; Gaps 24;

QY	13	CGCCCTCGCTCCCGCAGAGTCCCTCGCGCAGCAGATGTGTGGGGTCCAGCCAC	72
DB	165	CTCCGGCGCTCCCGCAGCAGTCCCTCGCGCAGCAGATGTGTGGGGTCCAGCCAC	224
QY	73	GGCGGGACTATGGTGAATTCCTCGCGCTCAGCAGTCTCGCGCTCGCGCTTCCT	132
DB	225	GGCGGGACTATGGTGAATTCCTCGCGCTCAGCAGTCTCGCGCTCGCGCTTCCT	284
QY	133	GGTGGCCCTGGGATCACCACATAGCCATCGATTCGGGGAGCAGCCCTTGAACCGGG	192
DB	285	GGTGGCCCTGGGATCACCACATAGCCATCGATTCGGGGAGCAGCCCTTGAACCGGG	344
QY	193	CATTGTGTGTCAAGAGGATCAGTCGAGATGCTGGCCAGCTACGGCTCGCGTACTC	252
DB	345	CATCGCTGAGTCAAGAGGATCAGTCGAGATGCTGGCCAGCTACGGCTCGCGTACTC	404

QY	253	CCTCATGAAGTCTTCTCACGGGTCCCATGAGTACTTCAAAAAATGTGGGCTGGTGTGT	312
DB	405	TTTGATGAAGTCTTCTCACGGGTCCCATGAGTACTTCAAAAAATGTGGGCTGGTGTGT	464
QY	313	GAACAGCAAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGTGGGCGCATCGC	372
DB	465	GAACAGCAAGAGAGACAGGACCAAGCCGTCCTGTGTATGGTGGTGGGCGCATCGC	524
QY	373	TGCGGTCTTTTCACACACTGATAGCTTATAGTATTTAGGATACATATCAATAAAT	432
DB	525	TGCGGTCTTTTCACACACTGATAGCTTATAGTATTTAGGATACATATCAATAAAT	584
QY	433	GCACCATGTGGAGAGTGGTGGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	492
DB	585	GCATCATGTGGATGAGTCTGTGGGAGCAAAAACAAGAGAGAGAGAGAGAGAGAG	644
QY	493	CTTTCTCTTTCATGACGCAATGCATGAGCCCATGCTGGCATCTCTTAAACACAAATA	552
DB	645	CTTTCTCTTTCATGACGCAATGCATGAGCCCATGCTGGCATCTCTTAAACACAAATA	704
QY	553	CAGTTTCTCTGTGGATGTGCTCAATCTCAGATGTGCATAGCTCAGGTGTTTGTAGC	612
DB	705	CAGTTTCTCTGTGGATGTGCTCAATCTCAGATGTGCATAGCTCAGGTGTTTGTAGC	764
QY	613	CATTCTCTTTCATGACGCAATGCATGAGCCCATGCTGGCATCTCTTAAACACAAATA	672
DB	765	CATTCTCTTTCATGACGCAATGCATGAGCCCATGCTGGCATCTCTTAAACACAAATA	824
QY	673	GTACATGGGCGCACTTGTGGCTGCACACCTGTGTGGTGGTGTGTGTGTGTGTGT	732
DB	825	GTACATGGGCGCACTTGTGGCTGCACACCTGTGTGGTGGTGTGTGTGTGTGTGT	884
QY	733	CGACATCATCTCTGACAGAGTGGCCCGGAGCTGGGGGGAGATGCAACATAGAAGAT	792
DB	885	CGACATCATCTCTGACAGAGTGGCCCGGAGCTGGGGGGAGATGCAACATAGAAGAT	944
QY	793	GCTGAGCTCTGTGGTGGCTTTTGGCTCTAAATCTGGCCACACAGAGATCAGTCGGCT	852
DB	945	GCTGAGCTCTGTGGTGGCTTTTGGCTCTAAATCTGGCCACACAGAGATCAGTCGGCT	1004
QY	853	TGTCACCTCTTTTCCCGGACCTTGTGTGGAGTCTTGTGAGCCACAGAGGAGTGGC	912
DB	1005	TGTCACCTCTTTTCCCGGACCTTGTGTGGAGTCTTGTGAGCCACAGAGGAGTGGC	1064
QY	913	GATTTTCACAGCCACATACCTGTGGTGCATGCAATGCAATGCAATGCAATGCAAT	972
DB	1065	GATTTTCACAGCCACATACCTGTGGTGCATGCAATGCAATGCAATGCAATGCAAT	1124
QY	973	TGCTGTGTATCTCTTTCGACAGAGATAAATCCCGAGCAACAACTGGTGGAGCAAG	1032
DB	1125	GGCTGTCTACCTGCTTTTGAAGAGATAAATCCCGAGCAACAACTGGTGGAGCAAG	1184
QY	1033	CACATGTCAGGCGACCCACATCAAGAGTTCATGCTGCTGCTGCTGCTGCTGCTGCT	1092
DB	1185	CACATGTCAGGCGACCCACATCAAGAGTTCATGCTGCTGCTGCTGCTGCTGCTGCT	1244
QY	1093	GCTCTGTTTGTGTATGTTTGGACACCCCAAGTCTCTGAGAGAAATCTGTAGACAT	1152
DB	1245	GCTCTGTTTGTGTATGTTTGGACACCCCAAGTCTCTGAGAGAAATCTGTAGACAT	1304
QY	1153	CGAGTGTGATCTTGTGCTTGCAGAACTCTGTGTGTGTGTGTGTGTGTGTGTGT	1212
DB	1305	TGGAGTGTGATCTTGTGCTTGCAGAACTCTGTGTGTGTGTGTGTGTGTGTGTGT	1364
QY	1213	CCAGTGTGATCTTGTGCTTGCAGAACTCTGTGTGTGTGTGTGTGTGTGTGTGT	1272
DB	1365	CCAGTGTGATCTTGTGCTTGCAGAACTCTGTGTGTGTGTGTGTGTGTGTGTGT	1424
QY	1273	CTTGT	1332
DB	1425	CTTGT	1484
QY	1333	CCTACCTTACCTGGGGGTGACAGGTGGAGCCCTGGGGGTGGGGTCTCTCTGGGGGCT	1392

Db	1485	CTGCGCGTACCTCGGGGGTGACGAGGCACACTAGGTGTGGGTCCCTTCTAGCAGGGTT	1544
Qy	1393	TGTGGGAGAATCACCATGTCGCCATCGCTGGTGTATGTCTACGGGAAGCAGAAAAA	1452
Db	1545	TGTGGGAGAATCTACCATGGTTCGCCCTTCAGCATGCTATGCTATCGAABACAGAAABA	1604
Qy	1453	GAAGATGGAGAATGAGTGGCCACGAGGGGGGAAGACTCTGCCATGACAGCATGCTCTCC	1512
Db	1605	GAAGATGGGAAATGAGTCAAGCCACGAGGGGAGAAGACTCGGCCATGACCGACATGCTCTCC	1664
Qy	1513	GACAGAGGAGGTGACAGACATCTGGAAATGAGAGAGGAGAAATGAATTAAGCACGGGACG	1572
Db	1665	AAACAGAGGAGGTACAGACATCGTAGAGATGAGAGAGAAATAGATAGCAGAGGCTGC	1724
Qy	1573	CCATGGGCATCTGAGGAGCGGTGAGTCAGGATGACACTTCGGCATCATCTCTCCCTCTC	1632
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Qy	1633	CCATCGTATTTTGTTCCTTTTTTTTGTGTTTTGT-TTGGTAATGAAGAGGCTTCGATTT	1691
Db	1784	CCATCAAGTTGTTTTCTGTTGTTTAAATTTTATCTTGGTATGAAGAGGCTTGATTT	1843
Qy	1692	AAAGGTTTCGTGCAATCTCTAGCATATCGGTATGCTCACATGACGGGGGACCTAG	1751
Db	1844	AGAGGTTTCGTATAAATTCCTAGCATCTAGGTATGCT-CACCGATGACGGGACCTGA	1901
Qy	1752	TGATGCTCTTACTGTTGCTATGTAAACAAACGAAACAACTGACTTCATACCCCTGC	1811
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Qy	1812	CTCACGAAAAACCAAAAGACACAGCTCCCTCACGGTTGACGTTGTGTCTCTCTCCCTCGG	1871
Db	1957	TTCA-TAAACCCCAAAGATAGAGTGCCTCTGGTCAACGTTT---CTACTCCCTTGG	2011
Qy	1872	ACATCTCTCTC-TTGGAAACCAAGGACTGACGTGTGCCATCGGGCTCGGTCAACCTGC	1930
Db	2012	ACAATCTCCACTTTGGAAACCAAGGACTG-----	2041
Qy	1931	ACAGCAGGCACAGACTCTCTGTCGCCCTTCATCGCTCTTAAGATCAACAGGTAAAA	1990
Db	2042	-----GGCCAGACTTTTCTGTTTCATGTTTGCTCTCTCTTAGAATCAACAGTTGAAG	2095
Qy	1991	CTCGGCTTCCTTTGATTTGCTTCCAGTACATGGCCGTACAAAGAGATGGAGCCCGGT	2050
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Db	2164	GTTGGGCCCCAGGCTGCAGCCACAGTCTCCCTGTTCCACAGAGAGGGCTGGTGCCCT	2223
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Db	2224	GCTGGGCCAACGTAGTGGGAATTTAATCTCTCTGTAGAAATTTGGGTCACTCA-----	2274
Qy	2231	GGGCGACGAACACTGACATGGTTGAATGATAGCATTTCACTCTCGGTTCTCTAGATCTGA	2290
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Qy	2291	GCAAGCTGTGAGTTCTCACCCCGCACCGGTGATATATAGAGCTAACTTTTTTAAATGTCT	2350
Db	2327	-----CCGCACCCACAGTGTATATACATGAGCTGACTTTTTTTCAGAGCTGTC	2372
Qy	2351	ACAAAAGCGATCTCCAGATTTCCAGACCCCTGCGCATGACTTTTTTCTCGAAGGCTTGCTTT	2410
Db	2373	CCGCAGTGTGAGCTTCCAGTGTACACACCT-CCGCATGAGTTTCCCTTGAAGGCTTGGCTT	2431
Qy	2411	TCCTCTGCTTCTCTGAAGTTCGCAATTAGAGCGAGTCAATGGAGCATCTCTAACTTGCA	2470

Db	2432	T-AC	CGCCTTCCCTGAGAGATGGCCACTAGAGCGAG--AAGTGGAGCGGTTCTAACTGTCCA	2488
Qy	2471	T-----	TTTAGTATTTTACAGTGAACCTGAAGCTTTAAAGTCTCATCCAGCAT	2515
Db	2489	TTTCTCTAACTGTC	CAATTTTCGTTTTTACAGTGGACAAAGCTTTAAAGTCGTAATCTAGCAT	2548
Qy	2516	TCTAATGCCAGGTTGCTGTAGG	TAACTTTTGAAGTAGATATATTAACCTGGTTCTGCTAT	2575
Db	2549	CCTAATGCCAGGTC	TGTCTGTAACCTTCTGATGTAGATGTGCCGCCATATTT	2601
Qy	2576	CCTTAGTCTAACTCTCGCGGTACAGGTAA	TGAGAATGTACTACGGTACTTCCCTCCCCAC	2635
Db	2602	-----	CTGCAGGACAGGTAACCGAG--TGTACTATGTGTACTCCCTC-----	2640
Qy	2636	ACCATAGATAAGCAAGACATTTTAT	-AACGNATACAGAGTCACCTATGTGGTCTCCCTC	2694
Db	2641	-CCACACCATAAAGCAAGACATTTTAAACAGTATCA	AAAGTCCACTATGTGATAC-CCCG	2698
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AX698612				
LOCUS AX698612 1568 bp DNA linear PAT 02-APR-2003				
DEFINITION Sequence 1 from Patent WO02072079.				
ACCESSION AX698612				
VERSION AX698612.1 GI:29499421				
KEYWORDS Homo sapiens (human)				
SOURCE Homo sapiens				
ORGANISM Homo sapiens				
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS Nuernberg, P.				
TITLE Agent for promoting bone formation and for use in osteoporosis therapy				
JOURNAL Patent: WO 02072079-A 1 19-SEP-2002;				
FEATURES Uni Charite Medizinische Fakultae der Humboldt-Uni zu Berlin (DE)				
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ORIGIN				
Query Match 52.5%; Score 1546.6; DB 6; Length 1568;				
Best Local Similarity 99.4%; Pred. No. 0;				
Matches 1552; Conservative 0; Mismatches 10; Indels 0; Gaps 0;				
Qy	18	CTGCGCTCCCGCAGAGTCCCTTCGCGGACAGAGATGTGTGGGGTCAGCCACACGGCGG	77	
Db	4	CTAGCTCCCGCAGAGTCCCTTCGCGGACAGAGATGTGTGGGGTCAGCCACACGGCGG	63	
Qy	78	GGACTATGTGAAATTCCTCGCGGCTCACGCATCTAGGCCCTCATCCGTTCTTGGTGC	137	

Db 64 GGACTATGTTGAAATTCGGCGCTCAGCACTACTGGCCCTGATCGGTTCTTGTTGC 123  
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 Db 124 CCTGGGATACCAACATAGCATCGACTTGGGGAGCAGCCCTTGAACCGGGCATG 183  
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RESULT 11  
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 LOCUS BD187385 1568 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Method for testing anti-osteoporosis agent.  
 ACCESSION BD187385  
 VERSION BD187385.1 GI:32997124  
 KEYWORDS JP 2003009871-A/2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1568)  
 AUTHORS Furukawa,H., Matsui,H., Kawaida,R. and Otsuka,T.  
 TITLE Method for testing anti-osteoporosis agent  
 JOURNAL Patent: JP 2003009871-A 2 14-JAN-2003;  
 Sankyo Company Limited  
 COMMENT OS Homo sapiens  
 PN JP 2003009871-A/2  
 PD 14-JAN-2003  
 PF 14-JUN-2001 JP 2001180142  
 PI hidehiko furukawa,hideki matsui,remi kawaida,toshiaki otsuka  
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ORIGIN  
 Query Match 52.5%; Score 1546.6; DB 6; Length 1568;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1552; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 18 CTCGCTCCCCGACAGATCCCTCGCGGACAGATGTGTGGGTGAGCCACCGCGG 77  
 Db 4 CTCAGCTCCCCGACAGATCCCTCGCGGACAGATGTGTGGGTGAGCCACCGCGG 63  
 QY 78 GGACTATGTTGAAATTCGGGGCTCAGCACTACTGCCCCCTGATCCGGTCTTGTGTC 137  
 Db 64 GGACTATGTTGAAATTCGGGGCTCAGCACTACTGCCCCCTGATCCGGTCTTGTGTC 123

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## RESULT 12

AF274753  
LOCUS  
DEFINITION  
Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds.  
ACCSSION  
AF274753  
VERSION  
AF274753.1 GI:9502216  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1568)  
Ho, A.M., Johnson, M.D. and Kingsley, D.M.  
Role of the mouse ank gene in control of tissue calcification and arthritis  
JOURNAL  
Science 289 (5477), 265-270 (2000)  
MEDLINE  
20355194  
PUBMED  
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REFERENCE  
2 (bases 1 to 1568)  
Kingsley, D.M., Ho, A.M. and Johnson, M.D.  
Direct Submission  
Submitted (05-JUN-2000) Department of Developmental Biology and Howard Hughes Medical Institute, Stanford University, Beckman Center B300, Stanford, CA 94304-5327, USA

FEATURES  
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## gene

## CDS

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## ORIGIN

Query Match 52.5%; Score 1546.6; DB 9; Length 1568;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1552; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Method for testing anti-osteoporosis agent.  
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VERSION JP 2003009871-A/1.  
KEYWORDS JP 2003009871-A/1.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 2737)  
AUTHORS Furukawa, H., Matsui, H., Kawaida, R. and Otsuka, T.  
TITLE Method for testing anti-osteoporosis agent  
JOURNAL Patent: JP 2003009871-A 1 14-JAN-2003;  
Sankyo Company Limited  
COMMENT OS Mus musculus  
FN JP 2003009871-A/1  
PD 14-JAN-2003  
PF 14-JUN-2001 JP 2001180142  
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CC CC  
FH Key Location/Qualifiers  
FT CDS (7)..(1482).







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REFERENCE			
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AUTHORS	Nuernberg, P.		
TITLE	Agent for promoting bone formation and for use in osteoporosis therapy		
JOURNAL	Patent: WO 02072079-A 2 19-SEP-2002;		
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Nuernberg, P.  
Agent for promoting bone formation and for use in osteoporosis therapy  
Patent: WO 02072079-A 2 19-SEP-2002;  
Uni Charite Medizinische Fakultae der Humboldt-Uni zu Berlin (DE)  
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VERSION	AC016649.4	11 unordered pieces.	
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	DOE Joint Genome Institute.		
JOURNAL	Sequencing of Human Chromosome 5		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 165671)		
TITLE	DOE Joint Genome Institute.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint		
AUTHORS	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		

COMMENT

On Apr 20, 2001 this sequence version replaced gi:7711590.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov  
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Project Information  
Center Project Name: 193053  
Center clone name: RPI-1\_14312  
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Summary Statistics  
Consensus quality: 152857 bases at least Q40  
Consensus quality: 156684 bases at least Q30  
Consensus quality: 157624 bases at least Q20  
Estimated insert size: 154000; pulse field gel estimation  
Quality coverage: 5.96 in Q20 bases; sum-of-contigs estimation  
Quality coverage: 5.57 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 11 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

- \* 1 1134: contig of 1134 bp in length
- \* 1135 1234: gap of unknown length
- \* 1235 2945: contig of 1711 bp in length
- \* 2946 3045: gap of unknown length
- \* 3046 4302: contig of 1257 bp in length
- \* 4303 4402: gap of unknown length
- \* 4403 5438: contig of 1036 bp in length
- \* 5439 5538: gap of unknown length
- \* 5539 7157: contig of 1619 bp in length
- \* 7158 7257: gap of unknown length
- \* 7258 9959: gap of unknown length
- \* 9960 11943: contig of 1985 bp in length
- \* 11944 12043: gap of unknown length
- \* 12044 21909: contig of 9866 bp in length
- \* 21910 22009: gap of unknown length
- \* 22010 40513: contig of 18404 bp in length
- \* 40514 40515: gap of unknown length
- \* 40516 68716: contig of 28203 bp in length
- \* 68717 68816: gap of unknown length
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FEATURES

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ORIGIN

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QY 2286 TCTGAGCAGCTGTCAGTTCTCACCCCGACCGTGTATATACATGAGCTAACTTTTAAA 2345
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Db 130440 TTGTCAAAAAGCGCATCTCCAGATTCAGACCCCTGCGCATGACTTTTCTGAAGGCTT 130499
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Db 130500 GCTTTTCCCTCGCCTTCTCGAAGGTCGCATTAGCGAGTCAATGAGGATCCTAACT 130559
QY 2466 TTGCATTTTGTGTTTACAGTGAATGAGCTTTAAGTCTCATCCAGATTTCTAATGCCA 2525
Db 130560 TTGCATTTTGTGTTTACAGTGAATGAGCTTTAAGTCTCATCCAGATTTCTAATGCCA 130619
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Db 130620 GGTGCTGTAGGTAACCTTTTGAAGTAGATATATTAAGTCTGCTTCTGCTATCCTTAGTCAT 130679
QY 2586 AACTCTGGGTACAGGTAATTTGAGAACTGACTACGGTACTTCCCTCCACACCATACGAT 2645
Db 130680 AACTCTGGGTACAGGTAATTTGAGAACTGACTACGGTACTTCCCTCCACACCATACGAT 130739
QY 2646 AAAGCAAGACATTTTATACGATACAGAGTCACTATGTGCTCTCTCCCTGAAATTAACGCA 2705
Db 130740 AAAGCAAGACATTTTATACGATACAGAGTCACTATGTGCTCTCTCCCTGAAATTAACGCA 130799
QY 2706 TTCGAAATCCATGCACTGATATATTTTCTAAGTTTGGAAAGCAGGTTTTTCCCTTT 2765
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Job time : 11409 secs

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Db 130920 CCTTAAACAAAATAATTTTAAAGATATAAATATATGCTGTATATGTTATGTAATTTATT 130979
QY 2886 TTAGGCTATATACATTTTCTTATTTTTCGATTTTCAATAAAATGTTCTTAATACAAA 2943
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